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Amendment to the Drawing

The attached sheets of Drawings includes Amendments to Figures 2-12. As requested by the Examiner, original Figures 2 and 4 were removed from the Drawing and are now included in the specification as Appendices G and H, respectively. The remaining Figures 3 and 5-12 were renumbered as Figures 2-10, so that figures are continuously numbered.

Attachment: Replacement Sheets

Remarks

Claims 50-69 and 82-106 are pending in the application. Claims 53, 54, 57, and 58 have been withdrawn from consideration by the Examiner. Claims 50-52, 55, 56, 59-69, and 82-106 are rejected by the Examiner.

Claims 50-95 have been canceled. Claims 96, 97, 100, 101, 104, 105, and 106 have been amended, and new claim 107 has been added. Support for amended claim 96 and new claim 107 can be found in the specification in paragraphs 46, 48, and 96 and in Example 1. Claims 97, 105, and 106 have been amended to correct the dependencies of those claims. Claims 100 and 101 were amended to correct the numbering within those claims.

Applicant submits that no new matter has been added by the present Amendment.

Applicant specifically reserves the right to pursue the subject matter of the original and previously presented claims in a related application; the present Amendment is introduced for the sole purpose of focusing the issues in this case and speeding its progress toward allowance.

Applicant respectfully requests reexamination and reconsideration of the present case, as amended. Each of the rejections levied in the Office Action is addressed individually below.

Objection to the specification. The Examiner has objected to the disclosure because pages 31 and 33-35 disclose nucleic acid sequences, but do not disclose embedded sequence identifiers (e.g., "SEQ ID NO:") as required by 37 C.F.R. § 1.821(d). As requested by the Examiner, Applicant has amended the specification to include embedded sequence identifiers. Applicant, therefore, respectfully requests that the rejection be removed.

The Examiner has further objected to the disclosure because it contains an embedded hyperlink and/or other form of browser-executable code. As requested by the Examiner, Applicant has amended the specification to remove the hyperlink. Applicant, therefore, respectfully requests that the objection be removed.

The Examiner has further objected to the Drawing, and this objection is addressed in more detail below. However, the Amendment to the Drawing has necessitated Amendments to the specification. As requested by the Examiner, original Figures 2 and 4 were removed from the Drawing and are now included in the Specification as Appendices G and H, respectively. The remaining original Figures 3 and 5-12 were renumbered as Figures 2-10, so that figures remain continuously numbered. The specification was Amended to correct the numbering of figures throughout the specification.

II. Objection to the drawing. The Examiner has objected to Figures 2 and 4. In particular, the Examiner states that Figures 2 and 4 are merely text lists of viral genes or components, and that they should be moved into the specification as tables and deleted as figures. Furthermore, the Examiner states that the remaining figures should be amended so that their numbering is continuous.

As requested by the Examiner, Applicant has amended the Drawing to remove Figures 2 and 4 and renumbered the remaining figures. In addition, Applicant has amended the specification to remove the legends to Figures 2 and 4 and to renumber the legends to the remaining figures. Furthermore Applicant has amended the specification to include Appendices G and H, which correspond to original Figures 2 and 4. Finally, Applicant has amended the specification to correct all references to figure numbers. Applicant, therefore, respectfully requests that the objection be removed.

- III. Rejection under 35 U.S.C. § 102(b) as being anticipated by Spitsin et al. (Proc. Natl. Acad. Sci., USA, 96: 2549-53, 1999). Claims 50-52, 55, 56, 59-69, 84, and 85 are rejected under 35 U.S.C. § 102(b) as being anticipated by Spitsin et al. (Proc. Natl. Acad. Sci., USA, 96: 2549-53, 1999). The Examiner states that Spitsin et al. teaches a vector in which the full-length cDNA of the RNA4 gene has been substituted into a tobacco mosaic virus vector. Thus, the Examiner states that the vector of Spitsin et al. anticipates the present claims. Claims 1-95 have been canceled by the present Amendment; therefore, Applicant respectfully submits that the rejection is rendered moot by the present Amendment.
- No. 6,858,426). Claims 50, 55, 56, 66, 68, and 86 are rejected under 35 U.S.C. § 102(e) as being anticipated by Zhu et al. (U.S. Patent No. 6,858,426). The Examiner states that embodiments outside of the elected species were discovered in the search for the elected species. In particular, the Examiner states that Zhu et al. teaches a viral vector comprising portions of several plant viruses, specifically the cauliflower mosaic virus (CaMV) 35S enhancer and promoter, the alfalfa mosaic virus RNA4 leader sequence, the Grapevine leafroll virus (type 2) coat protein gene, and the CaMV 35S 3' untranslated region. Thus, the Examiner states that the viral vector of Zhu et al. anticipates the present claims. Claims 1-95 have been canceled by the present Amendment; therefore, Applicant respectfully submits that the rejection is rendered moot by the present Amendment.

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V. Rejection under 35 U.S.C. § 112, first paragraph. Claims 50-52, 55, 56, 59-69, and 82-106 are rejected under 35 U.S.C. § 112, first paragraph, as failing to comply with the written description requirement. In particular, the Examiner uses two references to suggest that "the mere presence of expressed components of a virus together is not sufficient to predict function, given any sort of change or mutation." Thus, the Examiner argues, in the case of substituting one viral component for another, there can be no prediction of the ability of the new component to associate functionally with a second component of the original virus. The Examiner, therefore, concludes that the Applicant was not in possession of the full scope of the claimed invention at the time of filing. Applicant respectfully disagrees.

Applicant submits that the present specification demonstrates that (1) components of two different viruses (tobacco mosaic virus and alfalfa mosaic virus) are able to substitute for one another and can associate functionally with other viral components; and (2) such a system is able to successfully produce a desired protein. Furthermore, detailed methods for testing the ability of any viral components to be substituted for one another are described throughout the entire specification and are described further and demonstrated in the Examples; thus, Applicant submits that such methods are a matter of routine experimentation. Applicant reduces the invention to practice and describes methods by which any viral components can be tested for utility in accordance with the present invention. Applicant, therefore, respectfully submits that Applicant was in possession of the full scope of the claimed invention at the time of filing.

However, solely in order to further prosecution, Applicant has amended claim 96 to recite "tobacco mosaic virus" instead of "plant virus," and has added new claim 107, which recites "alfalfa mosaic virus." As discussed above, Applicant has clearly demonstrated that components of tobacco mosaic virus and alfalfa mosaic virus are able to substitute for one another and can associate functionally with other viral components in accordance with the present invention. Applicant, therefore, requests that this rejection be removed.

VI. Rejection under 35 U.S.C. § 112, second paragraph. Claims 94, 95, and 104 are rejected under 35 U.S.C. § 112, second paragraph, as being indefinite for failing to point out and distinctly claim the subject matter which Applicant regards as the invention. In particular, the Examiner states that there is insufficient antecedent basis for the phrase "the first and second polypeptides" in claims 94 and 95. Claims 94 and 95 are canceled by the present Amendment;

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therefore, Applicant respectfully submits that the rejection is rendered moot by the present Amendment.

The Examiner further states that the phrase, "proteins of pharmaceutical interest" in claims 95 and 104 is indefinite because it is not clear what this phrase means. Thus, claim 104 has been amended to recite, "therapeutically active proteins," as stated in paragraph 61 of the specification. Applicant submits that "therapeutically active proteins" in accordance with the present invention may include any of the proteins described in paragraphs 59-66 of the specification. Applicant, therefore, respectfully requests that the rejection be removed.

Applicant therefore respectfully submits that the present case is in condition for allowance. A Notice to that effect is respectfully requested.

If, at any time, it appears that a phone discussion would be helpful, the undersigned would greatly appreciate the opportunity to discuss such issues at the Examiner's convenience. The undersigned can be contacted at (617) 248-5000.

Please charge any fees that may be required for the processing of this Response, or credit any overpayments, to our Deposit Account No. 03-1721.

Respectfully submitted,

Cameron M. Luitjens, Ph.D.

Registration Number: 58,674

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Date: March 12, 2007

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APPENDIX A

DNA Viruses

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Circular dsDNA Viruses

Family: Caulimoviridae

Genus: <u>Badnavirus</u>

Type species: commeling yellow mottle virus

Genus: Caulimovirus

Type species: cauliflower mosaic virus

Genus "SbCMV-like viruses"

Type species: Soybean chloroticmottle virus

Genus "CsVMV-like viruses"

Type species: Cassava vein mosaicvirus

♦ Genus "RTBV-like viruses"

Type species: Rice tungro bacilliformvirus

Genus: "Petunia vein clearing-like viruses"

Type species: <u>Petunia vein clearing virus</u>

Circular ssDNA Viruses

Family: Geminiviridae

Genus: <u>Mastrevirus</u> (Subgroup | Geminivirus)

Type species: maize streak virus

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Genus: Curtovirus (Subgroup II Geminivirus)

Type species: beet curly top virus

Genus: <u>Begomovirus</u> (Subgroup III Geminivirus)

Type species: bean golden mosaic virus

RNA Viruses

ssRNA Viruses

Family: <u>Bromoviridae</u>

Genus: Alfamovirus

Type species: alfalfa mosaic virus

Genus: <u>llarvirus</u>

Type species: tobacco streak virus

Genus: <u>Bromovirus</u>

Type species: brome mosaic virus

Genus: Cucumovirus

Type species: <u>cucumber mosaic virus</u>

Family: Closteroviridae

Genus: Closterovirus

Type species: beet yellows virus

Genus: Crinivirus

Type species: Lettuce infectious yellows virus

Family: Comoviridae

Genus: Comovirus

Type species: cowpea mosaic virus

Genus: Fabavirus

Type species: broad bean wilt virus 1

Genus: Nepovirus

Type species: tobacco ringspot virus

Family: <u>Potyviridae</u>

Genus: Potyvirus

Type species: potato virus Y

Genus: <u>Rymovirus</u>

Type species: ryegrass mosaic virus

Genus: Bymovirus

Type species: <u>barley yellow mosaic virus</u>

Family: <u>Sequiviridae</u>

Genus: Sequivirus

Type species: parsnip yellow fleck virus

Genus: Waikavirus

Type species: rice tungro spherical virus

Family: Tombusviridae

Genus: <u>Carmovirus</u>

Type species: carnation mottle virus

Genus: <u>Dianthovirus</u>

Type species: carnation ringspot virus

Genus: Machlomovirus

Type species: maize chlorotic mottle virus

Genus: Necrovirus

Type species: tobacco necrosis virus

Genus: <u>Tombusvirus</u>

Type species: tomato bushy stunt virus

Unassigned Genera of ssRNA viruses

Genus: Capillovirus

Type species: apple stem grooving virus

Genus: Carlavirus

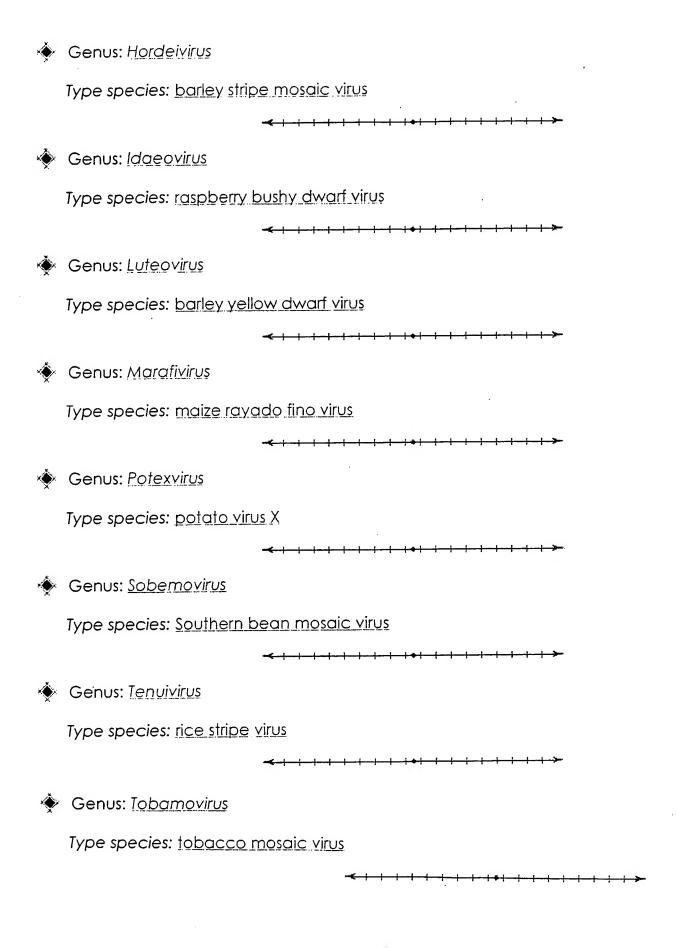
Type species: <u>carnation latent virus</u>

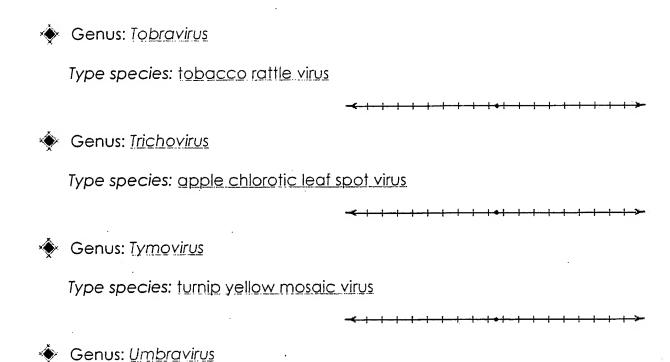
Genus: <u>Enamovirus</u>

Type species: pea enation mosaic virus

Genus: Furovirus

Type species: soil-borne wheat mosaic virus





Negative ssRNA Viruses

Order: MononegaviralesFamily: Rhabdoviridae

Genus Cytorhabdovirus

Type species: carrot mottle virus

Type Species lettuce necrotic yellows virus

Genus: Nucleorhabdovirus

Type species: potato yellow dwarf virus

Negative ssRNA Viruses

Family: Bunyaviridae

Genus: Tospovirus

Type species: tomato spotted wilt virus

dsRNA Viruses

Family: <u>Partitiviridae</u>

Genus: Alphacryptovirus

Type species: white clover cryptic virus 1

Genus: <u>Betacryptovirus</u>

Type species: white clover cryptic virus 2

Family: Reoviridae

Genus: Fijivirus

Type species: Fiji disease virus

Genus: Phytoreovirus

Type species: wound tumor virus

Genus: Oryzavirus

Type species: rice ragged stunt virus

Unassigned Viruses

- Genome ssDNA
 - Species banana bunchy top virus
 - Species <u>coconut foliar decay virus</u>
 - Species <u>subterranean clover stunt virus</u>
- Genome dsDNA
 - Species <u>cucumber vein yellowing virus</u>
- Genome <u>dsRNA</u>
 - Species tobacco stunt virus
- Genome ssRNA
 - Species Garlic viruses A,B,C,D
 - Species grapevine fleck virus
 - Species <u>maize white line mosaic virus</u>
 - Species olive latent virus 2
 - Species <u>ourmia melon virus</u>
 - Species <u>Pelargonium zonate spot virus</u>

Satellites and Viroids

- Satellites
 - ssRNA Satellite Viruses
 - Subgroup 2 Satellite Viruses

Type species: tobacco necrosis satellite

- Satellite RNA
 - Subgroup 2 B Type mRNA Satellites

 - Subgroup 3 C Type linear RNA Satellites
 Subgroup 4 D Type circular RNA Satellites

Viroids

Type species: potato spindle tuber viroid

KOMSSIVYTGPIKVQQMKNFIDSLVASLSAAVSNLVKILKDTAAIDLETR TMV - KR TMV-RAK KQMSSIVYTGPIKVQQMKNFIDSLVASLSAAVSNLVKILKDTAAIDLETR KQMSSIVYTGPIKVQQMKNFIDSLVASLSAAVSNLVKILKDTAAIDLETR TMV-vul KOMCSIVYTGPLKVQQMKNFIDSLVASLSAAVSNLVKILKDTAAIDLETR TOMV KOMHAMVYTGPLKVQQCKNYLDSLVASLSAAVSNLKKIIKDTAAIDLETK **PMMV** KQMASVVYTGSLKVQQMKNYVDSLAASLSATVSNLCKSLKDEVGYDSDSR **TMGMV** NKMASIVYSGPLOVOOMONYVDSLAASLSATVSNLKKLVKDSSVGFQDSL TMV-OB KSMSSAVYTGPLKVQQMKNYMDYLSASISATVSNLCKVLKDVYGVDPESA ORSV GTMMSAVYTGSIKVQQMKNYIDYLSASLAATVSNLCKVLRDVHGVDPESQ TVCV CR-TMV GTMMSAVYTGSIEVROMKNYIDYLSASLSATVSNLCKVLRDVHGVDPESQ RMV-SH GAMMSAVYTGKIKVQQMKNYVDYLSASLSATVSNLCKVLRDVHGVDPESQ GAMMSAVYTGKIKVQQMKNYVDYLSASLSATVSNLCKVLRDVHGVDPESQ CRMV GAMMSAVYTGKIKVOOMKNYVDYLSASLSATVSNLCKVLRDVHGVDSESQ TMV - CG KTITPVVYTGTIRERQMKNYIDYLSASLGSTLGNLERIVRSDWNGTEESM **CGMMV** KTITPVVYTGTIRERQMKNYIDYLSASLGSTLGNLERIVRSDWNGTEESM CGMMV - W <u>CFM</u>MV KTITPVIYTGPIRVRQMANYLDYLSANLAATIGILERIVRSNWSGN-EVV KSITPVIYTGPIRVRQMANYLDYLSASLTATIGNLERIVSSSWTGENELV YCGMMV QKPVNIVYTGEVQICQMQNYLDYLSASLVACISNLKKYLQDQWLNPGEKF SHMV

5 3

QKFGVLDVASRKWLIKPTAKSHAWGVVETHARKYHVALLEYDE-QGVVTC TMV KR QKFGVLDVASRKWLIKPTAKSHAWGVVETHARKYHVALLEYDE-QGIVTC TMV-RAK P03586 TMVQKFGVLDVASRKWLIKPTAKSHAWGVVETHARKYHVALLEYDE-QGVVTC QKFGVLDVASKRWLVKPSAKNHAWGVVETHARKYHVALLEHDE-FGIITC TOMV EKFGVYDVCLKKWLVKPLSKGHAWGVVMDSDYKCFVALLTYDG-ENIVCG PPMV EKVGVWDVTLKKWLLKPAAKGHSWGVVLDYKGKMFTALLSYEG-DRMVTE **TMGMV** SKVGVFDVRKKMWLIKPTLKNHSWGVVQKFDGKCFLALLSYHN-ELPICD TMV OB EKSGVYDVVKGKWIIKPKDKCHAWGVADLNNGEKVIVLLEWAD-GFPIC-ORSV . EKSGVWDVRRGRWLLKPNAKSHAWGVAEDANHKLVIVLLNWDD-GKPVCD TVCV EKSGVWDVRRGRWLLKPNAKSHAWGVAEDANHKLVIVLLNWDD-GKPVCD CR-TMV EKSGVWDVRRGRWLLKPNAKCHAWGVAEDANHKLVIVLLNWDE-GNPVCD RMV-SH EKSGVWDVRRGRWLLKPNAKCHAWGVAEDANHKLVIVLLNWDE-GKPVCD CRMV EKSGVWDVRRGRWLLKPNAKCHAWGVAEDANHKLVIVLLNWDE-GKPVCD TMV-CG OTFGLYDCEKCKWLLLPAEKKHAWAVVLASDDTTRIIFLSYDESGSPIID CGMMV CGMMV - W OTFGLYDCEKCKWLLLPAEKKHAWAVVLASDDTTRIIFLSYDESGSPIID QTYGLFDCQANKWILLPSEKTHSWGVCLTMDDKLRVVLLQYDSAGWPIVD **CFMMV** QTYGLFDCQADKWILQPTERTHSWGVCLTMDDKLRIVLLQYDEFDWPIVD YCGMMV QKIGVWDNLNNKWIVVPQKKKYAWGLAADVDGNQKTVILNYDEHGMPILE SHMV

101

TMV KR -DNWRRVAVSSESVVYSDMAKLRTLRRLLRNGEPHVSSAKVVLVDGVPGC TMV-RAK -DDWRRVAVSSESVVYSDMAKLRTLRRLLRDGEPHVSNAKVVLVDGVPGC P03586 TMV-DDWRRVAVSSESVVYSDMAKLRTLRRLLRNGEPHVSSAKVVLVDGVPGC -DNWRRVAVSSESVVYSDMAKLRTLRRLLKDGEPHVSSAKVVLVDGVPGC TOMV -ETWRRVAVSSESLVYSDMGKIRAIRSVLKDGEPHISSAKVTLVDGVPGC PPMV -SDWRRVAVSSDTMVYSDIAKLQNLRKTMRDGEPHEPTAKMVLVDGVPGC **TMGMV** -ADWSKVAVSNESMVYSDMAKLRVLRKSIGEMPISVSSAKVTLVDGVPGC TMV OB -GDWRRVAVSSDSLIYSDMGKLOTLLRCLKDGEPVLRMPKVTLVDGVLGC ORSV -ETWFRVAVSSDSLIYSDMGKLKTLTSCSPNGEPPEPNAKVILVDGVPGC TVCV -ETWFRVAVSSDSLIYSDMGKLKTLTTCSPNGEPPEPNAKVILVDGVPGC CR-TMV RMV-SH -ETWFRLAVSSDSLVYSDMGKLKTLTACCRDGEPPEPTAKVVLVDGVPGC -ETWFRLAVSSDSLVYSDMGKLKTLTSCCRDGEPPEPTAKLVLVDGVPGC CRMV -ETWFRLAVSSDSLVYSDMGKLKTLTACCRDGEPPEPTAKVVLVDGVPGC TMV-CG KKNWKRFAVCSETKVYSVIRSLEVLNKE----AIVDPGVHITLVDGVPGC **CGMMV** KKNWKRFAVCSETKVYSVIRSLEVLNKE----AIVDPGVHITLVDGVPGC CGMMV-W KSFWKAFCVCADTKVFSVIRSLEVLSAL----PLVEPDAKYVLIDGVPGC CFMMV KSSWKAFCVSADTKVFSIIRSLEVLSSL----PLSDPTAKFTLIDGVPGC YCGMMV -KSYVRLVVSTDTYLFTVVSMLGYLRHL----DQKKPTATITLVDGVPGC SHMV

AAEMIRRRANS-SGIIVATKDNVKTVD GKTKEILSRVNFDEDLILVP GKTKEILSRVNFDEDLILVPGKQAAEMIRRRANS-SGIIVATKDNVRTVD TMV-RAK P03586 TMVGKTKEILSRVNFDEDLILVPGKQAAEMIRRRANS-SGIIVATKDNVKTVD GKTKEILSRVNFEEDLILVPGRQAAEMIRRRANA-SGIIVATKDNVRTVD TOMV GKTKEILSRVNFDEDLVLVPGKQAAEMIRRRANS-SGLIVATKENVRTVD PPMV GKYKGDFERFDLDEDLILVPGKQAAAMIRRRANS-SGLIRATMDNVRTVD **TMGMV** GKTKEILRRVNFSEDLVLVPGKEAAAMIRKRANQ-SGNIVANNDNVKTVD TMV OB GKTKEILETVNFDEELILVPGKEACKMIIKRANK-SGHVRATKDNVRTVD ORSV GKTKEIIEKVNFSEDLILVPGKEASKMIIRRANQ-AGVIRADKDNVRTVD TVCV GKTKEIIEKVNFSEDLILVPGKEASKMIIRRANH-AGVIRADKDNVSTVD CR-TMV GKTKEILEKVNFSEDLVLVPGKEASKMIIRRANQ-AGVTRADKDNVRTVD RMV-SH GKTKEILEKVNFSEDLVLVPGKEASKMIIRRANQ-AGITRADKDNVRTVD CRMV GKTKEILEKVNFSEDLVLVPGKEASKMIIRRANQ-AGIIRADKDNVRTVD TMV-CG GKTAEIIARVNWKTDLVLTPGREAAAMIRRRACALHKSPVATNDNVRTFD **CGMMV** GKTAEIIARVNWKTDLVLTPGREAAAMIRRRACALHKSPVATNDNVRTFD CGMMV-W GKTQEIISSADFKTDLILTPGKEAAAMIRRRANMKYRSPVATNDNVRTFD CFMMV GKTQEIINSADFKTDLILTPGKESAAMIRRRANAKFRGCVATNDNVRTFD YCGMMV GKTQEILSRFDANSDLILVQGREACEMIRRRAND-NVPGSATKENVRTFD SHMV

201

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25:

IPYINRVSGFPYPAHFAKLEVDEVETRRTTLRCPADVTHYLNRRYEGFVM TMV KR IPYINRVSGFPYPAHFSKLEVDEVETRRTTLRCPADVTHYLNRRYEGFVV TMV-RAK P03586 TMVIPYINRVSGFPYPAHFAKLEVDEVETRRTTLRCPADVTHYLNRRYEGFVM IPYINRVTGFPYPAHFAKLEVDEVETRRTTLRCPADVTHFLNQRYEGHVM TOMV IPYINRVATFPYPKHLSQLEVDAVETRRTTLRCPADITFFLNQKYEGQVM PPMV IPFINRVQNFPYPKHFEKLQVDEVEMRRTTLRCPGDVNFFLQSKYEGAVT **TMGMV** IPYINRVQNFPFPQHFSKLIVDETEKRRTTLRCPVDVTHFLNQCYDGAVT TMV OB IPFINRVANFPYPKHFGHTCLHRREVRRLSLRCPADVTHFMNSKYDGKFL ORSV IPFICRVANFPYPAHFAKLVADEKEVRRVTLRCPADVTYFLNKKYDGAVM TVCV IPFICRVANFPYPAHFAKLVADEKEVRRVTLRCPADVTYFLNKKYDGAVM CR-TMV IPFICRVANFPYPSHFAKLVVDEKEDRRVTLRCPADVTYFLNTRYDGSVM RMV-SH IPFICRVANFPYPAHFAKLVVDEKEDRRVTLRCPADVTYFLNQKYDGSVL CRMV IPFICRVANFPYPKHFAKLVVDEKEDRRVTLRCPADVTFFLNKKYDGAVL TMV-CG IPFINRVMNFDYPKELRTLIVDNVERRYVTHRCPRDVTSFLNTIYKAAVA **CGMMV** IPFINRVMNFDYPKELRTLIVDNVERRYVTHRCPRDVTSFLNTIYKAAVA CGMMV-W IPFINRVMNFDYPLELRKIIVDTVEKRYTSKRCPRDVTHYLNEVYSSPVC **CFMMV** IPFINRVMNFDYPLELKKIIVDDVEKRYTSKRCPRDVTHYLNEVYAAPVT YCGMMV IPFINRVMNFSIPDNLAKLYYDEIVSRDTTKRCPLDVTHFLNSVYEKRVM SHMV

301

TMV KR STSSVKKSVSQEMVGGAAVINP-ISKPLHGKILTFTQSDKEALLSRGYS-TMV-RAK STSSVKKSVSQEMVSGAAVINP-ISKPLHGKILTFTQSDKEALLSRGYS-P03586 TMVSTSSVKKSVSQEMVGGAAVINP-ISKPLHGKILTFTQSDKEALLSRGYS-TOMV CTSSEKKSVSQEMVSGAASINP-VSKPLKGKILTFTQSDKEALLSRGYA-

Tobamovirus Helicase--Alignment

```
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                                  VSKPLKGKVITFTQSDKSLLLSRGYE-
PPMV
          TTSTVQRSVSSEMIGGKGVLNS-VSKPLKGKIVTFTQADKFELEEKGYK-
TMGMV
TMV OB
          TTSKTORSVGLEVVGGAAVMNP-VTKPLKGKIVTFTQSDKLTMLSRGYQ-
          CTNDVIRSVDAEVVRGKGVFNP-KSKPLKGKIITFTQSDKAELNERGYEE
ORSV
          CTSAVERSVKAEVVRGKGALNP-ITLPLEGKILTFTQADKFELLEKGYK-
TVCV
CR-TMV
          CTSAVERSVKAEVVRGKGALNP-ITLPLEGKILTFTQADKFELLEKGYK-
          CTSSVERSVSAEVVRGKGALNP-ITLPLEGKILTFTQADKFELLDKGYK-
RMV-SH
          CTSSVERSVSAEVVRGKGALNP-ITLPLEGKILTFTQADKFELLDKGYK-
CRMV
          CTSSVERSVSAEVVRGKGALNP-ITLPLEGKILTFTQADKFELLDKGYK-
TMV-CG
          TTSPVVHSVKAIKVSGAGILRP-ELTKIKGKIITFTQSDKQSLIKSGYN-
CGMMV
          TTSPVVHSVKAIKVSGAGILRP-ELTKIKGKIITFTQSDKQSLIKSGYN-
CGMMV - W
          TTSPVVHSVTTKKIAGVGLLRP-ELTALPGKIITFTQNDKQTLLKAGYA-
CFMMV
          TSSAVVHSVSQKKIAGVGLLRP-ELTSLEGKIITFTQSDKQTLLKAGYE-
YCGMMV
          SYSNVQRSLECKMISGKAKINDYRSILAEGKLLTFTQEDKEYLLKAGFK-
SHMV
```

351

----DVHTVHEVQGETYSDVSLVRLTPTPVSIIAGDSPHVLVALSRHTC TMV KR ----EVHTVHEVQGETYSDVSLVRLTPTPISIIAGDSPHVLVALSRHTC TMV-RAK P03586 TMV-----DVHTVHEVQGETYSDVSLVRLTPTPVSIIAGDSPHVLVALSRHTC ----DVHTVHEVOGETYADVSLVRLTPTPVSIIARDSPHVLVSLSRHTK TOMV ----DVHTVHEVQGETFEDVSLVRLTPTPVGIISKQSPHLLVSLSRHTR PPMV ----NVNTVHEIOGETFEDVSLVRLTATPLTLISKSSPHVLVALTRHTK **TMGMV** -----DVNTVHEIQGETYEEVSLVRLTPTPIHIISRESPHVLVGLTRHTR TMV OB VSTFGEINTVHEIQGETFEDVSVVRLTPTALELISKSSPHVLVALTRHTK ORSV TVCV ----DVNTVHEVOGETYEKTAIVRLTSTPLEIISSASPHVLVALTRHTT ----DVNTVHEVQGETYEKTAIVRLTSTPLEIISRASPHVLVALTRHTT CR-TMV ----DVNTVHEVQGETYEKTAIVRLTATPLEIISRASPHVLVALTRHTT RMV-SH ----DVNTVHEVQGETYEKTAIVRLTATPLEIISRASPHVLVALTRHTT CRMV ----DVNTVHEVQGETYEKTAIVRLTATPLEIISRASPHVLVALTRHTT TMV-CG ----DVNTVHEIQGETFEETAVVRATPTPIGLIARDSPHVLVALTRHTK **CGMMV** ----DVNTVHEIQGETFEETAVVRATPTPIGLIARDSPHVLVALTRHTK CGMMV-W ----DVNTVHEVQGETYEETSVVRATATPIGLISRKSPHVLVALSRHTK **CFMMV** ----DVNTVHEVQGETYECTSVVRATATPIGLISRKSPHVLVALSRHTK YCGMMV ----DVNTVHEAQGETYRDVNLIRVTATPLTIVSAGSPHVTVALSRHTN SHMV

401

TMV KR SLKYYTVVMDPLVSIIRDLEKLSSYLLDMYKVDA TMV-RAK SLKYYTVVMDPLVSIIRDLEKLSSYLLDMYKVDA P03586 TMVSLKYYTVVMDPLVSIIRDLEKLSSYLLDMYKVDA SLKYYTVVMDPLVSIIRDLERVSSYLLDMYKVDA TOMV SIKYYTVVLDAVVSVLRDLECVSSYLLDMYKVDV PPMV SFKYYTVVLDPLVQIISDLSSLSSFLLEMYMVEA TMGMV CFKYYTVVLDPLVKLVRDLECVSNFLLDVYMVDS TMV OB SFKYYCVVLDPLVKVCSDLSKVSDFILDMYKVDA ORSV CCKYYTVVLDPMVNVISEMEKLSNFLLDMYRVEA TVCV RCKYYTVVLDPMVNVISEMEKLSNFLLDMYRVEA CR-TMV RCKYYTVVLDPMVNVISELGKLSNFLLEMYKVES RMV-SH RCKYYTVVLDPMVNVISELGKLSNFLLEMYKVES CRMV RCKYYTVVLDPMVNVISEMEKLSNFILDMYKVES TMV-CG AMVYYTVVFDAVTSIIADVEKVDQSILTMFATTV **CGMMV** AMVYYTVVFDAVTSIIADVEKVDQSILTMFATTV CGMMV-W AMTYYTVTVDPVSCIIADLEKVDQSILSMYASVA **CFMMV** YCGMMV TMTYYTVTVDPVSCIIADLEKVDQSILSMYATVA SHMV RFVYYTVVPDVVMTTVQKTQCVSNFLLDMYAVAY

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Last Updated: Thur., May 31, 2001

Tobamovirus RNA dependent RNA p. .nerase

A three-dimensional structure of a RNA-dependent RNA polymerase, that encoded by poliovirus, has been reported by <u>Hansen et al</u>. The alignment used for tree construction is enhanced below by the amino acid sequence of the poliovirus RdRP aligned to the tobamoviral RdRp's. A 3D line is provided that identifies the helices (upper case Roman) and beta-structure elements (numerals) described in that report. The footnote line refers to notes at the bottom that relate to functional or structural comments.

```
TMV-vul
          --MQFYYDKCLPGNSTMMNNFD---AVTMRLTDISLNVKDCILDMSKSVA
TMV-Rak
          --MQFYYDKCLPGNSTMMNNFD---AVTMRLTDISLNVKDCILDMSKSVA
          --MQFYYDKCLPGNSTMMNNFD---AVTMRLTDISLNVKDCILDMSKSVA
TMV-WANG
TOMV-L
          --MOFYYDKCLPGNSTLLNNYD---AVTMKLTDISLNVKDCILDMSKSVA
          --MOFYYDKCLPGNSTMMNNFD---AVTMRLTDISLNVKDCILDMSKSVA
TMV - KR
          --MQYYYDKCLPGNSTILNEYD---AVTMQIRENSLNVKDCVLDMSKSVP
PMMV
          PDLOFYYDVCLPGNSTILNKYD---AVTMRLRDNSLNVKDCVLDFSKSIP
TMGMV
          --MOFYYDTLLPGNSTILNEYD---AVTMNLRENNLNVKDCTIDFSKSVS
<u>ORSV</u>
          --MQFYYDALLPGNSTILNEFD---AVTMNLRDISLNVKDCRIDFSKSVQ
TVCV
          --MOFYNDTLLPGNSTILNEYD---AVTMNLRDISLNVKDCRIDFSKSVQ
CR-TMV
RMV-SH
          --MOFYYDTLLPGNSTILNEFD---AVTMNLRDISLNVKDCRIDFSKSVQ
          --MQFYYDTLLPGNSTILNEFD---AVTMNLRDISLNVKDCRIDFSKSVQ
CRMV
          --MQFYYDTLLPGNSTILNEFD---AVTMNLRDISLNVKDCRIDFSKSVQ
TMV - CG
TMV-OB
          QDLQFYYDKCLPGNSTVLNEFD---AVTMNCSDISLNVKDCVLDFSKSVP
          --MQEFYDRCLPGNSFVLNDFD---AVTMRLRDNEFNLQPCRLTLSNLDP
<u>CGMMV</u>
          TDMQEFYDRCLPGNSFVLNDFD---AVTMRLRDNEFNLQPCRLTLSNLDP
CGMMV-W
          --MONFYDACLPGNSFVLNDYD---SVTMRLVDNEINLQPCRLTLSKADP
CFMMV
          TDMQSFYDACLPGNSFVLNDYD---SVTMRLADNEFNLQPCRLTLSKADP
YCGMMV
          --LQYFYDSWLPGNSFVQNNHD---QWSIISSDINLHSEAVRLDMNKRH-
SHMV
POLIORDRP GEIQWMRPSKEVGYPIINAPSKTKLEPSAFHY-VFEGVKEPAVLTKNDPR
3D
                                      11
Footnote
                                           1
          AP---KDOIK-PLIPMVRTAAEMPRQTGLLENLVAMIKRNFNAPELSGII
TMV VUL
          AP---KDOIK-PLIPMVRTAAEMPROTGLLENLVAMIKRNFNAPELSGII
TMV-RAK
TMV WANG
        AP---KDQIK-PLIPMVRTAAEMPRQTGLLENLVAMIKRNFNAPELSGII
TOMV L
          AP---KDVKP-TLIPMVRTAAEMPRQTGLLENLVAMIKRNFNSPELSGVV
TMV-KR
          AP---KDOIK-PLIPMVRTAAEMPRQTGLLENLVAMIKRNFNAPELSGII
          LP---RESET-TLKPVIRTAAEKPRKPGLLENLVAMIKRNFNSPELVGVV
PMMV
TMGMV SPA MP---KEVKP-CLEPVLRTAAEPPRAAGLLENLVAMIKRNFNAPDLTGTI
ORSV
          VP---ROOEE-FFTPVIRTAAERPRSAGLLENLVAMIKRNFNSPDLTGIL
          LP---KEQPI-FLKPKIRTAAEMPRTAGLLENLVAMIKRNMNAPDLTGTI
TVCV
          LP---KEQPI-FLKPKIRTAAEMPRTAGLLENLVAMIKRNMNAPDLTGTI
CR-TMV
          VP---KERPV-FMKPKLRTAAEMPRTAGLLENLVAMIKRNMNAPDLTGTI
RMV-SH
          VP - - - KERPV - FMKPKLRTAAEMPRTAGLLENLVAMIKRNMNAPDLTGTI
CRMV
          LP---RERPI-FMKPKLRTAAEMPRTAGLLENLVAMIKRNMNAPDLTGTI
TMV-CG
          LP---RDNTKVPMTPVIRTAAERPRSQGLLENLVAMIKRNFNSPELSGTV
TMV OB
          VPALIKNEAQNFLIPVLRTACERPRIPGLLENLVAMIKRNMNTPDLAGTV
CGMMV
          VPALVKSEAQNFLIPVLRTACERPRIPGLLENLVAMIKRNMNTPDLAGTV
CGMMV-W
          VTESLKMEKKEFLIPLGKTATERPRIPGLLENLIAIVKRNFNTPDLAGSL
CFMMV
          VAESIKLERKNIDKLDLKTATERPRIPGFLENLVAIVKRNFNTPDLAGVL
YCGMMV
          ----IPRTKGEFLRPLLNTAVEPPRIPGLLENLLALIKRNFNAPDLAGQL
SHMV
POLIORDRP L---K-TNFEEAIFSKYVGNKITEVDEHMKEAVDHYAGQLMSLDINTEQ
            3D
Footnote
          DIENTASLVVDKFFDSYLLKE-----KRKPNKNVSLFSRESLNRWLEKQE
TMV VUL
          DIENTASLVVDKFFDSYLLKE-----KRKPNKNVSLFSRESLNRWLEKQE
TMV-RAK
          DIENTASLVVDKFFDSYLLKE-----KRKPNKNVSLFSRESLNRWLEKQE
TMV WANG
          DIENTASLVVDKFFDSYLLKE-----KRKPNKNFSLFSRESLNRWIAKQE
TOMV L
          DIENTASLVVDKFFDSYLLKE-----KRKPNKNVSLFSRESLNRWLEKQE
TMV-KR
          DIEDTASLVVDKFFDAYLIKE-----KKKP-KNIPLLSRASLERWIEKQE
PMMV
TMGMV SPA DIESTASVVVDKFFDSYFIKK-----EKYTKNIAGVMTKDSMMRWLENRK
          DIEDTAELVVNKFWDAYIIDE-LSGGNVTPM-----TSDAFHRWMAKQE
ORSV
          DIEDTASLVVEKFWDSYVDKE-FSGTNEMTM-----TRESFSRWLSKQE
TVCV
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```
SGTNEMTM-----TRESFSRWLSKQE
          DIEDTASLVVEKFWDSYIDKI
          DIEDTASLVVEKFWDAYVVKE-FSGTDGMAM-----TRESFSRWLSKQE
RMV-SH
          DIEDTASLVVEKFWDAYVVKE-FSGTDGMAM----TRESFSRWLSKQE
CRMV
          DIEDTASLVVEKFWDAYVVKE-FSGTDGMAM-----TRESFSRWLSKQE
TMV-CG
          DMENTASVVADRFFDSYFLKDKLSGCSLGDSGGKNIIDRQALIRWMEKQE
TMV OB
          DITMMSISIVDNFFSSFVRDE-V---LLDHLDCVRASSIQSFSDWFSCQP
CGMMV
          DITNMSISIVDNFFSSFVRDE-V---LLDHLDCVRASSIQSFSDWFSCQP
CGMMV-W
          DISSISKGVVDNFFSTFLRDE-Q---LADHLCKVRSLSLESFSAWFDNQS
CFMMV
          DIDTISKSVVDNFFTTFLRDE-Q---LSDHLVRVRSCSLESFSAWFHNOA
YCGMMV
          DYDFLSRKVCDGFFGKLLPPD-VEASELLRLPVDHMYSVQNFDDWLNKQE
SHMV
POLIORDRP MCLEDAMYGTDGLEALDLSTS----AGYPYVAMGKKKRDILN-----
Footnote
          OVTIGOLADFDFVDLPAVDQYR-HMYKAQPKQKLDTSIQTEYPA-LQTIV
TMV VUL
          RVTIGOLADFDFVDLPAVDQYR-HMIKAQPKQKLDTSIQTEYPA-LQTIV
TMV-RAK
          QVTIGQLADFDFVDLPAVDQYR-HMIKAQPKQKLDTSIQTEYPA-LQTIV
TMV WANG
          OVTIGOLADFDFVDLPAVDQYR-HMIKAQPKQKLDLSIQTEYPA-LQTIV
TOMV L
          QVTIGQLADFDFVDLPAVDQYR-HMIKAQPKQKLDTSIQTEYPA-LQTIV
TMV-KR
          KSTIGQLADFDFIDLPAVDQYR-HMIKQQPKQRLDLSIQTEYPA-LQTIV
PMMV
TMGMV SPA EVLLDDLANYNFTDLPAIDQYK-HMIKAQPKQKLDLSIQNEYPA-LQTIV
          KSTIRQLADFDFVDLPAIDQYK-HMIKAQPKQKLDLSPQDEYAA-LQTIV
ORSV
          SSTVGQLADFNFVDLPAVDEYK-HMIKSQPKQKLDLSIQDEYPA-LQTIV
TVCV
          SSTVGQLADFNFVDLPAVDEYK-HMIKSQPKQKLDLSIQDEYPA-LQTIV
CR-TMV
          SSTVGQLADFNFVDLPAVDEYK-HMIKSQPKQKLDLSIQDEYPA-LQTIV
RMV-SH
          SSTVGQLADFNFVDLPAVDEYK-HMIKSQPKQKLDLSIQDEYPA-LQTIV
CRMV
          SSTVGQLADFNFVDLPAVDEYK-HMIKSQPKQKLDLSIQDEYPA-LQTIV
TMV-CG
          KSTIGQLADYDFVDLPAIDQYR-HIIKSQPKQKLDLSIQSEYPS-LQTIV
TMV OB
          TSAVGQLANFNFIDLPAFDTYM-HMIKRQPKSRLDTSIQSEYPA-LQTIV
CGMMV
          TSAVGQLANFNFIDLPAFDTYM-HMIKRQPKSRLDTSIQSEYPA-LQTIV
CGMMV-W
          TCALGQLSNFDFVDLPPVDVYN-HMIKRQPKSKLDTSIQSEYPA-LQTIV
CFMMV
          TAAMGQLANFDFSDLPPVDMYT-HMIKRQPKSKLDTSIQSEYPA-LQTIV
YCGMMV
          PGVVGQLANWDHIGMPAADQYR-HMIKRTPKAKLDLSIQSEYPA-LQTIV
SHMV
POLIORDRP KQTRDTKEMQKLLDTYGINLPLVTYVKDELRSKTKV-EQGKSRLIEASSL
Footnote
          YHSKKINAIFGPLFSELTRQLLDSVDSSRFLFFTRKTPAQIEDFFGDLDS
TMV VUL
          YHSKKINAIFGPLFSELTRQLLDSVDSSRFLFFTRKTPAQIEDFFGDLDS
TMV-RAK
TMV WANG YHSKKINAIFGPLFSELTRQLLDSVDSSRFLFFTRKTPAQIEDFFGDLDS
          YHSKKINAIFGPLFSELTRQLLDSIDSSRFLFFTRKTPAQIEDFFGDLDS
TOMV L
          YHSKKINAIFGPLFSELTRQLLDSVDSSRFLFFTRKTPAQIEDFFGDLDS
TMV-KR
          YHSKKINALFGPVFSELTRQLLETIDSSRFMFYTRKTPTQIEEFFSDLDS
PMMV
TMGMV SPA YHSKQINGILAG-FSELTRLLLEAFDSKKFLFFTRKTPEQIQEFFSDLDS
          YHSKOINAIFGPLFAELTRQLLERIDSSKFLFYTRKTPEQIEEFLSDLDS
ORSV
          YHSKKINAIFGPMFSELTRMLLERIDSSKFLFYTRKTPAQIEDFFSDLDS
TVCV
          YHSKKINAIFGPMFSELTRMLLERIDSSKFLFYTRKTPAQIEDFFSDLDS
CR-TMV
          YHSKKINAIFGPMFSELTRMLLERIDTSKFLFYTRKTPTQIEEFFSDLDS
RMV-SH
          YHSKKINAIFGPMFSELTRMLLETIDTSKFLFYTRKTPTQIEEFFSDLDS
CRMV
          YHSKKINAIFGPMFSELTRMLLERIDTSKFLFYTRKTPTQIEEFFSDLDS
TMV-CG
          YHSKKINALFGPIFSELTROMLSAIDTSRYLFFTRKTPEQIEEFFSDLDA
TMV OB
          YHPKVVNAVFGPVFKYLTTKFLSMVDSSKFFFYTRKKPEDLQEFFSDLSS
CGMMV
          YHPKVVNAVFGPVFKYLTTKFLSMVDSSKFFFYTRKKPEDLQEFFSDLSS
CGMMV-W
          YHSKLVNAVFGPVFRYLTSEFLSMVDNSKFFFYTRKLRMICKFLFPHFPN
CFMMV
          YHSKLVNAVFGPVFRYLTSEFLSMVDNSKFFFYTRKTPEDLQSFFSTLSA
YCGMMV
          YHSKHVNAVFGPIFSCLTERLLSVVDPLRFKFFTRTTPADLEFFFRDMVV
SHMV
POLIORDRP NDSVAMRMAFGNLYAAFHK------NPGVITGSAVGCDPDLFWSKIPV
          ---BBBBB-CCCCCCCC-----DDDDDDD
3D
                             aaaaaaa
Footnote
          HVPMDVLELDISKYDKSQNEFHCAVEYEIWRRLGFEDFLGEVWKQGHRKT
TMV VUL
          HVPMDVLELDISKYDKSQNEFHCAVEYEIWRRLGFEDFLGEVWKQGHRKT
TMV-RAK
TMV WANG HVPMDVLELDISKYDKSQNEFHCAVEYEIWRRLGFEDFLGEVWKQGHRKT
          HVPMDVLELDVSKYDKSQNEFHCAVEYEIWRRLGLEDFLAEVWKQGHRKT
TOMV L
          HVPMDVLELDISKYDKSQNEFHCAVEYEIWRRLGFEDFLGEVWKQGHRKT
TMV - KR
          NVPMDILELDISKYDKSQNEFHCAVEYEIWKRLGLDDFLAEVWKHGHRKT
PMMV
TMGMV SPA HVPMDVLELDISKYDKSQNEFHCAVEYEIWKRLGLNEFLAEVWKQGHRKT
```

```
AVEYFIWEKLGLNGFLEEVWKQGHRKT
          TVPMEALVLDISKYDKSQNEL
          TQAMEILELDISKYDKSQNEFHCAVEYKIWEKLGIDEWLAEVWKQGHRKT
TVCV
          TOAMEILELDISKYDKSQNEFHCAVEYKIWEKLGIDEWLAEVWKQGHRKT
CR-TMV
          SQAMEILELDISKYDKSQNEFHCAVEYKIWEKLGIDEWLAEVWRQGHRKT
RMV-SH
          SQAMEILELDISKYDKSQNEFHCAVEYKIWEKLGIDDWLAEVWRQGHRKT
CRMV
          SQAMEILELDISKYDKSQNEFHCAVEYKIWEKLGIDDWLAEVWRQGHRKT
TMV-CG
          HQPMEVLELDVSKYDKSQNEFHCAVEYEIWKRLGIDEFLAEVWKQGHRKT
TMV OB
          HSDYEILELDVSKYDKSQSDFHFSIEMAIWEKLGLDDILAWMWSMGHKRT
CGMMV
          HSDYEILELDVSKYDKSQSDFHFSIEMAIWEKLGLDDILAWMWSMGHKRT
CGMMV-W
          KQEYEILELDVSKYDKSQNDFHQAVEMLIWERLGLDDILARIWEMGHKKT
CFMMV
          KESYEILELDVSKYDKSQTDFHQAVEMLIWERLGLDDVLARIWEMGHKKT
YCGMMV
          -GDMEILELDISKYDKSQNKFHFEVEMRIWEMLGIDKYIEKVWENGHRKT
SHMV
POLIORDRP LMEEKLFAFDYTGYDASLSPAWFEALEMVLEKIGFGDRVDYIDYLNHSHH
          D---11111111-EEEE---FFFFFFFFFFF--GGGGGG------
3D
                   4
                          6
Footnote
          TLKDYTAGIKTCIWYQRKSGDVTTFIGNTVIIAACLASMLPME-----K
TMV VUL
          TLKDYTAGIKTCIWYQRKSGDVTTFIGNTVIIAACLASMLRME----K
TMV-RAK
          TLKDYTAGIKTCIWYQRKSGDVTTFIGNTVIIAACLASMLPME-----K
TMV WANG
          TLKDYTAGIKTCLWYQRKSGDVTTFIGNTVIIASCLASMLPME----K
TOMV L
          TLKDYTAGIKTCIWYQRKSGDVTTFIGNTVIIAACLASMLPME-----K
TMV-KR
          TLKDYTAGIKTCLWYQRKSGDVTTFIGNTIIIAACLSSMLPME----R
PMMV
TMGMV SPA TLKDYIAGIKTCLWYQRKSGDVTTFIGNTVIIAACLGSMLPME-----K
          SLKDYTAGIKTCLWYQRKSGDVTTFIGNTVIIAACLASMIPMD-----K
ORSV
          TLKDYTAGVKTCLWYQRKSGDVTTFIGNTIIIAACLSSMIPMD-----K
TVCV
          TLKDYTAGIKTCLWYQRKSGDVTTFIGNTIIIAACLSSMIPMD-----K
CR-TMV
          TLKDYTAGIKTCLWYQRKSGDVTTFIGNTIIIAACLSSMIPMD-----K
RMV-SH
          TLKDYTAGIKTCLWYQRKSGDVTTFIGNTIIIAACLSSMIPMD-----K
CRMV
          TLKDYTAGIKTCLWYQRKSGDVTTFIGNTIIIAACLSSMIPMD-----K
TMV-CG
          TLKDYTAGIKTCLWYQRKSGDVTTFIGNTVIIAACMASMLPME-----K
TMV OB
          ILQDFQAGIKTLIYYQRKSGDVTTFIGNTFIIAACVASMLPLD-----K
CGMMV
          ILQDFQAGIKTLIYYQRKSGDVTTFIGNTFIIAACVASMLPLD-----K
CGMMV-W
          HISDFQAGIKTLIYYQRKSGDVTTFIGNTFIIAACVASMVPLS-----R
CFMMV
          SISDFQAGIKTVIYYQRKSGDVTTFIGNTFIIAACVASMIPLS-----R
YCGMMV
          HLRDYTAGIKTVIEYQRKSGDVTTFIGNTIIIAACLCSILPME----K
SHMV
POLIORDRP LYKNKTYCVKGGM----PSGCSGTSIFNSMINNLIIRTLLLKTYKGIDLD
          _____
3D
                                     5
                                                     aaaaaa
Footnote
          IIKGAFCGDDSLLYFPKGCEFPDV-QHSA--NLMWNFEAK-----LFKKQ
TMV VUL
          IIKGAFCGDDSLLYFPKGCEFPDI-QHSV--NLMWNFEAK----LFKKQ
TMV-RAK
          IIKGAFCGDDSLLYFPKGCEFPDV-QHSA--NLMWNFEAK-----LFKKQ
TMV WANG
          LIKGAFCGDDSLLYFPKGCEYPDI-QQAA--NLMWNFEAK-----LFKKQ
TOMV L
          IIKGAFCGDDSLLYFPKGCEFPDV-QHSA--NLMWNFEAK----LFKKQ
TMV-KR
          LIKGAFCGDDSILYFPKGTDFPDI-QQGA--NLLWNFEAK----LFRKR
PMMV
TMGMV SPA VIKGAFCGDDSVLYFPKGLDFPDI-QSCA--NLMWNFEAK-----LYRKR
          VIKAAFCGDDSILDIPKGLDLPDI-QSEA--NLMWNFEAK----LYRKR
ORSV
          VIKAAFCGDDSLIYIPKGLDLPDI-QAGA--NLMWNFEAK----LFRKK
TVCV
          VIKAAFCGDDSLIYIPKGLDLPDI-QAGA--NLMWNFEAK----LFRKK
CR-TMV
          VIKAAFCGDDSLIYIPKGLDLPDI-QAGA--NLTWNFEAK----LFRKK
RMV-SH
          VIKAAFCGDDSLIYIPKGLDLPDI-QAGA--NLTWNFEAK----LFRKK
CRMV
          VIKAAFCGDDSLIYIPKGLDLPDI-QAGA--NLTWNFEAK----LFRKK
TMV-CG
          VIKAAFCGDDSLVYLPKGCELPNI-QSCA--NLMWNFEAK----LFKKT
TMV OB
          CFKASFCGDDSLIYLPKGLEYPDI-QATA--NLVWNFEAK----LFRKK
CGMMV
          CFKASFCGDDSLIYLPKGLEYPDI-QATA--NLVWNFEAK----LFRKK
CGMMV.-W
          SFKAAFCGDDSLIYMPPNLEYNDI-QSTA--NLVWNFEAK-----LYKKK
CFMMV
          SFKASFCGDDSLIYMPPGLEYPDI-QATA--NLVWNFEAK----LFKKR
YCGMMV
          VFKAGFCGDDSIIYLPRNLLYPDI-QSVS--NNMWNFEAK----LFKKL
SHMV
POLIORDRP HLKMIAYGDDVIASYPHEVDASLLAQSGKDYGLTMTPADKSAIFETVTWE
          222222---333333-----IIIIIIIIII-4444------
Footnote
                  44
                             9 9
          YGYFCGRYVIHHDRGCIVYYDPLKL-ISKLGAKHIKDWEHLEEFRRSLCD
TMV VUL
          YGYFCGRYIIHHDRGCIVYYDPLKL-ISKLGAKHIKDWEHLEEFRRSLCD
TMV-RAK
          YGYFCGRYVIHHDRGCIVYYDPLKL-ISKLGAKHIKDWEHLEEFRRSLCD
TMV WANG
          YGYFCGRYVIHHDRGCIVYYDPLKL-ISKLGAKHIKDWDHLEEFRRSLCD
TOMV L
          YGYFCGRYVIHHDRGCIVYYDPLKL-ISKLGAKHIKDWEHLEEFRRSLCD
TMV - KR
```

```
YGYFCGRYIIHHDRGCIVYYL KL-ISKLGAKHIKNREHLEEFRTSLCD
PMMV
TMGMV SPA YGYFCGRYIIHHDKGAIVYYDPLKL-ISKLGAKHIKDYDHLEELRVSLCD
          YGYFCARYIIHHDRGAIVYYDPLKL-ISKLGCKHIKSLDHLEEFRMSLCD
ORSV
          YGYFCGRYVIHHDRGAIVYYDPLKL-ISKLGCKHIRDVVHLEELRESLCD
TVCV
          YGYFCGRYVIHHDRGAIVYYDPLKL-ISKLGCKHIRDVVHLEELRESLCD
CR-TMV
          YGYFCGRYVIHHDRGAIVYYDPLKL-ISKLGCKHIRDEVHLEELRRSLCD
RMV-SH
          YGYFCGRYVIHHDRGAIVYYDPLKL-ISKLGCKHIRDEVHLEELRRSLCD
CRMV
          YGYFCGRYVIHHDRGAIVYYDPLKL-ISKLGCKHIRDEVHLEELRRSLCD
TMV-CG
          YGYFCGRYVIHHDRGAIVYVDPLKI-ISKLGAKHITDKEHLEEFRISLAD
TMV OB
          YGYFCGKYIIHHANGCIVYPDPLKL-ISKLGNKSLVGYEHVEEFRISLLD
CGMMV
          YGYFCGKYIIHHANGCIVYPDPLKL-ISKLGNKSLVGYEHVEEFRISLLD
CGMMV-W
          YGYFCGKYVIHHANGCIVYPDPLKL-ISKLGNKSLESYDHLEEFRISLMD
CFMMV
          YGYFCGKYVIHHSNGCIVYPDPLKL-ISKLGNKSLESYDHLEEFRISLMD
YCGMMV
          HGYFCGRYILRNGRYLRLLPDPLKI-ITKLGCKAIKDWDHLEEFRISMFD
SHMV
          NVTFLKRFFRADEKYPFLIHPVMPMKEIHESIRWTKDPRNTQDHVRSLCL
POLIORDRP
          3 D
                                                   88
                                                       8
              77
Footnote
          VAVSLNN-CAYYTQLDDAVWEVHKTAPPGSFVYKSLVKYLSDKVLFRSLF
TMV VUL
          VAVSLNN-CAYYTQLDDAVWEVHKTAPPGSFVYKSLVKYLSDKVLFRSLF
TMV-RAK
          VAVSLNN-CAYYTQLDDAVWEVHKTAPPGSFVYKSLVKYLSDKVLFRSLF
TMV WANG
          VAESLNN-CAYYTQLDDAVGEVHKTAPPGSFVYKSLVKYLSDKVLFRSLF
TOMV L
          VAVSLNN-CAYYTQLDDAVWEVHKTAPPGSFVYKSLVKYLSDKVLFRSLF
TMV-KR
          VAGSLNN-CAYYTHLNDAVGEVIKTAPLGSFVYRALVKYLCDKRLFQTLF
PMMV
TMGMV SPA VACSLGNWCLGFPQLNAAIKEVHKTAIDGSFAFNCVNKFLCDKFLFRTLF
          VSSSLNN-CALFGQLNDAIAEVHKTAVNGSFAFCSIVKYLSD????????
ORSV
          VASNLNN-CAYFSQLDEAVAEVHKTAVGGSFAFCSIIKYLSDKRLFRDLF
TVCV
          VASNLNN-CAYFSQLDEAVAEVHKTAVGGSFAFCSIIKYLSDKRLFRDLF
CR-TMV
          VTSNLNN-CAYFSQLDEAVAEVHKTAVGGAFVYCSIIKYLSDKRLFKDLF
RMV-SH
          VTSNLNN-CAYFSQLDEAVAEVHKTAVGGAFVYCSIIKYLSDKRLFKDLF
CRMV
          VTSNLNN-CAYFSQLDEAVAEVHKTAVGGAFVYCSIIKYLSDKRLFKDLF
TMV-CG
          VSKSLNN-CAYYAQLDEAVREVHKTAPPGSFVYKCIVKFLSNRVLFESLF
TMV OB
          VAHSLFN-GAYFHLLDDAIHELFPNAGGCSFVINCLCKYLSDKRLFRSLY
CGMMV
          VAHSLFN-GAYFHLLDDAIHELFPNAGGCSFVINCLCKYLSDKRLFRSLY
CGMMV-W
          VAKPLFN-AAYFHLLDDAIHEYFPSVGGSTFAISSLCKYLSNKQLFGSLF
CFMMV
          VAKPLFN-AAYFHLLDDAIHEYFPSVGGSSFAINSLCKYLSDKWLFRSLF
YCGMMV
          MACEYKN-CFGFDVLESAVKESFPKAEGCNVAFCAIYKFLSNKYLFRTLF
SHMV
POLIORDRP LAWHNGE-EEYNKFL------AKIRSVPIGRALLLPEYSTLYRRWL
          KKKK--L-LLLLLL------LLLL--MMMM-----NNNNNNNN
37)
                                                         0
                                                8
Footnote
TMV VUL
          ID
          IN
TMV-RAK
          ID
TMV WANG
TOMV L
          LD
TMV-KR
          ID
PMMV
          LE
TMGMV SPA LN
          ??
ORSV
          FV
TVCV
          FV
CR-TMV
          FV
RMV-SH
          FV
CRMV
          FV
TMV-CG
          F?
TMV OB
CGMMV
          ID
CGMMV - W
          ID
          IK
CFMMV
YCGMMV
          ΑK
          SD
SHMV
          DS
POLIORDRP
          NN
3D
Footnote
```

- Footnotes:
- 1. N-terminal residues interacting with the thumb.
- 4. Three aspartates involved in metal ion binding at the active site.
- 5. Determinant of preference for NTP over dNTP. Could interact with 2' OH of substrate NTP.
- 6. Caps a helical turn
- 7. beta-turn.
- 8. Interaction across interface I
- 9. Interaction across interface I with Arg 456
- 0. See 9.
- a. Extra residues are present between helix H and beta-2 for poliovirus and between helix D and helix C for tobamoviruses. Their sequence similarity (YKGID for polio vs. LDSID for ToMV) suggests that they may serve similar functions in providing part of Interface I.

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Tobamovirus Movement Protein

SHMV SKIST--LLAPEKFVKLSVSDKFKWKAPSRVCSIVQSDTISMTANGR-SL **CGMMV** SKVSVENSLKPEKFVKISWVDKLLPNYFSILKYLSITDFSVVKAQSYESL CGMMV-W ${ t SKVSVENSLKPEKFVKISWVDKLLPNYFSILKYLSITDFSVVKAQSYESL}$ C-CGMMV SSVGVKNVLKPNEFVKLSWVDRILPDMFTVYRYLSVTDYSVIKSKDSECL **CFMMV** SKVGVRNALKPEEFVKITWVDKLLPDAFTILKYLSITDYSVVQSKDYEHL YCGMMV SSVGVKNVLKPNEFVKLSWVDRILPDMFTVYRYLSVTDYSVIKSKDSECL **FPMV** VELKEPKOLKVNDFVKMSFADKILPRSLTRLRTVSISETNVVKLSGLGST TMV-CG ????MSYEPKVSDFLALTKKEEILPKAFTRLKTVSISTKDVISVKDSESL CRMV ????MSYEPKVSDFLALTKKEEILPKALTRLKTVSISTKDVISVKESESL CR-TMV ?MSIVSYEPKVSDFLNLSKKEEILPKALTRLKTVSISTKDIISVKESETL RMV-SH ????MSYEPKVSDFLALTKKEEILPKALTRLKTVSISTKDVISVKESESL TVCV ?MSIVSYEPKVSDFLNLSKKEEILPKALTRLKTVSISTKDIISVKESETL **TMGMV** MAVSLRDTVKISEFIDLSKQDEILPAFMTKVKSVRISTVDKIMAVKNDSL TMV-OB ---MSKAIVKIDEFIKLSKSEEVLPSAFTRMKSVRVSTVDKIMAKENDNI **PMMV** MALVVKDDVKISEFINLSAAEKFLPAVMTSVKTVRISKVDKVIAMENDSL ORSV MALVLRDSIKISEFINLSASEKLLPSALTAVKSVRISKVDKIISYENDTL TOMV-L MALVVKGKVNINEFIDLSKSEKLLPSMFTPVKSVMVSKVDKIMVHENESL TMV-vul MALVVKGKVNINEFIDLTKMEKILPSMFTPVKSVMCSKVDKIMVHENESL TMV-Rak MALVVKGKVNINEFIDLTKMEKILPSMFTPVKSVMCSKVDKIMVHENESL

51

SHMV30K FTFDVLKDVLKHA-EEYTYVDVLGVVLSGQWLLPKGTPGSAEIILLDSRL CGMMV30K VPVKLLRGV--DL-TKHLYVTLLGVVVSGVWNVPESCRGGATVALVDTRM CGMMV-W VPVKLLRGV--DL-TKHLYVTLLGVVVSGVWNVPESCRGGATVALVDTRM IPVDLLRGV--DL-SKSKYVTLVGVVISGVWTIPENCAGGATVALVDTRM C-CGMMV IPVDLLRGV--DF-SKSKYVTLVGVVISGVWTIPENCAGGATVALVDTRM CFMMV YCGMMV IPVDLLRGV--DL-SKSKYVTLVGVVISGVWTIPENCAGGATVALVDTRM FPMV VNLNILKGV--VLNSESKYVTIRGVVISGVWMVPEGGGGGATVTLMDRRM TMVCG CDIDLLVNV--PL-DKYRYVGVLGVVFTGEWLVPDFVKGGVTVSVIDKRL CRMV CDIDLLVNV--PL-DKYRYVGVLGVVFTGEWLVPDFVKGGVTVSVIDKRL CRTMV CDIDLLINV--PL-DKYRYVGILGAVFTGEWLVPDFVKGGVTISVIDKRL RMV-SH CDIDLLVNV--PL-DKYRYVGVLGVAFTGEWLVPDFVKGGVTVSVIDKRL TVCV CDIDLLINV--PL-DKYRYVGILGAVFTGEWLVPDFVKGGVTISVIDKRL TMGMVA 30KSDVDLLKGV--KL-VKKGYVCLADLVVSGEWNLPDNCRGGVSVCIVDKRM TMV OB SEVDLLKGV--KL-VKNGYVCLVGLVVSGEWNLPDNCRGGVSICLIDKRM **PMMV** SDVNLLKGV--KL-VKDGYVCLAGLVVSGEWNLPDNCRGGVSVCLVDKRM DRSV 30K SDIDLLKGV--KL-VENGYVCLAGLVVTGEWNLPDNCKGGVSICLVDKRM IMVL30K SEVNLLKGV--KL-IEGGYVCLVGLVVSGEWNLPDNCRGGVSVCMVDKRM **IMVOM30K** SEVNLLKGV--KL-IDSGYVCLAGLVVTGEWNLPDNCRGGVSVCLVDKRM **IMV-RAK** SEVNLLKGV--KL-IDSGYVCLAGLVVTGEWNLPDNCRGGVSVCLVDKRM

101

3HMV30K KGKASVLAVFNCRAATQEFQFLISPGYSLTCADALKKPFEISCNVIDLP CGMMV30K HSVAEGTICKFSAPATVREFSVRFIPNYSVVAADALRDPWSLFVRLSNVG :GMMV-W HSVAEGTICKFSAPATVREFSVRFIPNYSVVAADALRDPWSLFVRLSNVG :- CGMMV ${ t SMVDEGTICKFSVAASTRDFMVKLIPNYYVAASDASSKPWSIFVRVSGVR}$:FMMV SLVSEGTICKFSVSAASRDFTVKLIPNYYVTAADASSKPWSLFVRISGVR 'CGMMV ${ t SMVDEGTICKFSVAASTRDFMVKLIPNYYVLASDASSKPWSIFVRVSGVR}$ 'PMV KGFKNGLVAEFKTRASSRDFQFKFIPNYSMCVDDVKRAPWELFFKLVGVP MVCG ENSKECIIGTYRAAAKDKRFQFKLVPNYFVSVADAKRKPWQVHVRIQNLR !RMV ENSKECIIGTYRAAAKDRRFQFKLVPNYFVSVADAKRKPWQVHVRIQNLK !RTMV ANSKECVIGTYRAAAKSKRFQFKLVPNYFVSTVDAKRKPWQVHVRIQDLK MV-SH ENSRESMIGTYRAAAKDRRFQFKLVPNYFVSTADAKRKPWQVHVRIQNLK 'VCV VNSKECVIGTYRAAAKSKRFQFKLVPNYFVSTVDAKRKPWQVHVRIQDLK MGMVA 30KKRSKEATLGAYHAPACKKNFSFKLIPNYSITSEDAEKHPWQVLVNIKGVA MV OB QRHNEATLGSYTTKASKKNFSFKLIPNYSITSQDAERRPWEVMVNIRGVA VMM QRDDEATLGSYRTSAAKKRFAFKLIPNYSITTADAERKVWQVLVNIRGVA RSV 30K KRANEATLGSYHTSACKKRFTFKIIPNYSVTTADALKGIWQVMTNIRGVE MVL30K ERADEATLGSYYTAAAKKRFQFKVVPNYGITTKDAEKNIWQVLVNIKNVK MVOM30K ERADEATLGSYYTAAAKKRFQFKVVPNYAITTQDAMKNVWQVLVNIRNVK

TMV-RAK ERADEATLGSYYTAAAKKRF (VVPNYAITTQDAMKNVWQVLVNIRNVK

151 SHMV30K VKDGFTPLSVEIACLVQFSNCVITRSLTMKLKE-N--PATRTF---SAEE IKDGFHPLTLEVACLVATTNSIIKKGLRASVVE-SVVSSDQSI---VLDS CGMMV30K CGMMV - W IKDGFHPLTLEVACLVATTNSIIKKGLRASVVE-SVVSSDQSI---VLDS C-CGMMV IKEGFSPLTLEIASLVATTNSILKKGLRVSVLE-SVVGSDASI---NLDT **CFMMV** IKDGFSPLTLEIASLVATTNSILKKGLRVSVIE-SVVGSDASV---SLDT YCGMMV IKEGFSPLTLEIASLVATTNSILKKGLRVSVLE-SVVGSDASI---NLDT **FPMV** IEDGYYPLAIEIATLVEQSRTIINHGLRATILKRCDDISDLELPSADLDE TMVCG IEAGWQPLALEVVSVAMVTNNVVVKGLREKVIA-VNDPNVEGF-EGVVDD CRMV IEAGWQPLALEVVSVAMVTNNVVVKGLREKVIA-VNDPNVEGF-EGVVDD CRTMV IEAGWQPLALEVVSVAMVTNNVVMKGLREKVVA-INDPDVEGF-EGVVDE RMV-SH IEAGWQPLALEVVSVAMVTNNVVVKGLREKVIA-VNDPNVEGF-EGVVDD TVCV IEAGWQPLALEVVSVAMVTNNVVMKGLREKVVA-INDPDVEGF-EGVVDE TMGMVA 30KMEEGYCPLSLEFVSICVVHKNNVRKGLRERILS-VTDGSPIELTEKVVEE MSEGWCPLSLEFVSVCIVHKNNVRKGLREKVTA-VSEDDAIELTEEVVDE TMV OB **PMMV** MEKGFCPLSLEFVSVCIVHKSNIKLGLREKITS-VSEGGPVELTEAVVDE ORSV 30K MEKGFCPLSLEFVSICVVYLNNIKLGLREKILN-VTEGGPTELTEAVVDE MSAGYCPLSLEFVSVCIVYKNNIKLGLREKVTS-VNDGGPMELSEEVVDE TMVL30K TMVOM30K MSAGFCPLSLEFVSVCIVYRNNIKLGLREKITN-VRDGGPMELTEEVVDE TMV-RAK MSAGFCPLSLEFVSVCIVYRNNIKIGLREKITN-VRDGGPMELTEEVVDE

201

SHMV30K VDELLGSMTTLRSIEGLRKKKEP CGMMV30K LSEKVEPFFDKVPISAAVMARDP CGMMV-W LSEKVEPFFDKVPISAAVMARDP C-CGMMV VSDKVQPFFDSVPITAAVIARDR **CFMMV** LSEKVQPFFDSVPITASVVSRDR VSDKVQPFFDSVPITAAVIARDR YCGMMV **FPMV** SIELVSNSNIVSKRKTHKKGKKR TMVCG **FVDSVAAFKAVDTFRKKKKRIGG** CRMV FVDSVAAFKAIDSFRKKKKRIGG CRTMV **FVDSVAAFKAVDNFKRRKKKVEE** RMV-SH **FVDSVAAFKAIDSFRKKKKKIGG TVCV FVDSVAAFKAVDNFRKRKKKVEE** IMGMVA 30KFVDEVPMAVKLEKVPENKKEMVG TMV OB FIEAVPMARRLQNLRKPKYNKEK **PMMV** FIESVPMADRLRKFRNOSKKGSN DRSV 30K FVEKVPMAARLKSFRSVNKKKPS [MVL30K **FMENVPMSVRLAKFRTKSSKRGP** rmvom30K **FMEDVPMSIRLAKFRSRTGKKSD** CMV-RAK **FMEDVPMSIRLAKFRSRTGKKSV**

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Alignment of tobamovirus coat protei equences

SYSITTPSQFVFLSSAWADPIELINLCTNALGNQFQTQQARTVVQRQFSE

1

TMV-OM

SYSITTPSQFVFLSSAWADPIELINLCINALGNQFQTQQARTVVQRQFSE S34858 SYSITTPSQFVFLSSAWADPIELINLCINALGNQFQTQQARTVVQRQFSE S34857 S34856 SYSITTPSQFVFLSSAWADPIELINLCINALGNQFQTQQARTVVQRQFSE TMV-ER SYNITTPSQFVFLSSAWADPLELINLCTNALGNQFQTQQARTVVQRQFSE TMV-06 SYSITTPSHFVFLSSAWADPIELINLCTNALGNQFQTQQARTVVQRQFSE SYSITTPSQFVFLSSAWADPIELINLCTNALGNQFQTQQARTVVQRQFSE TMV-vul SYSITSPSQFVFLSSVWADPIELLNVCTSSLGNQFQTQQARTTVQQQFSE TMV-DA SYSITSPSQFVFLSSVWADPIELLNVCTNSLGNQFQTQQARTTVQQQFSE TOMV-L SYTVSSANOLVYLGSVWADPLELQNLCTSALGNQFQTQQARTTVQQQFSD ToMV-Kr PYTINSPSOFVYLSSAYADPVQLINLCTNALGNQFQTQQARTTVQQQFAD **TMGMV** TMV-OB PYTVTSPSQLVYFGSVWADPITFIDLCTVALGNQFQTQNARTTVQQQFSD AYTVSSANQLVYLGSVWADPLELQNLCTSALGNQFQTQQARTTVQQQFSD **PMMV** PYTVSSPNQLVYFGSVWADPIALIDLCTVSLGNQFQTQNARTTVQQQFSD PkMMV ORSV SYTITDPSKLAYLSSAWADPNSLINLCTNSLGNQFQTQQARTTVQQQFAD SYTITDPSKLAYLSSAWADPNSLINLCTNSLGNQFQTQQARTTVQQQFAD ORSV-F CR-TMV SYNITNPNQYQYFAAVWAEPIPMLNQCISALSQSYQTQAARDTVRQQFSN SYNITNPNQYQYFAAVWAEPIPMLNQCMSALSQSYQTQAARDTVRQQFSN <u>TVCV</u> SYNITNSNQYQYFAAVWAEPTPMLNQCVSALSQSYQTQAGRDTVRQQFAN RMV SYNITNSNQYQYFAAVWAEPTPMLNQCVSALSQSYQTQAGRDTVRQQFAN HRMV.GER SYNITNSNQYQYFAAVWAEPTPMLNQCVSALSQSYQTQAGRDTVRQQFAN HRMV.JAP SYNITNSNQYQFFAAVWAEPIAMLNQCVSALSQSYQTQAARDTVRQQFSN <u>WASAB</u>I TMV-CG SYNITSSNQYQYFAAMWAEPTAMLNQCVSALSQSYQTQAARDTVRQQFSN VYNITSSNQYQYFAAMWAEPTAMLNQCVSALSQSYQTQAARDTVRQQFSN CRMV VYNITSSNQYQYFAAMWAEPTAMLNQCVSALSQSYQTQAARDTVRQQFSN RMV-SH RMV-SH SYNITSSNOYOYFAAMWAEPTAMLNQCVSALSQSYQTQAARDTVRQQFSN SYNITSSNQYQYFAAMWAEPQAMLNQCVSALSQSYQTQAARDTVRQQFSN RMV-CAB **CGMMV** AYNPITPSKLIAFSASYVPVRTLLNFLVASQGTAFQTQAGRDSFRESLSA CGMMV-W AYNPITPSKLIAFSASYVPVRTLLNFLVASQGTAFQTQAGRDSFRESLSA C-CGMMV SYSTSGIRSLPAFAKSFYPFYDVYNLLVSAQGGALQTQNGKDILRESLTG SYSTSGLRSLPAYTKSFCPYYALYDLLVSAQGGALQTQNGKDILRDSING CFMMV SYSISSFRSLPAYTKSFYPFIEFYNLLVSSQGGALQTQNGKDISRESLNG YCGMMV SYSTSGIRSLPAFAKSFYPFYDVYNLLVSAQGGALQTQNGKDILRESLTG KGMMV PYSTSGIRSLPAFSKSFFPYLELYNLLITNQGAALQTQNGKDILRESLVG ZGMMV AYSIPTPSQLVYFTENYADYIPFVNRLINARSNSFQTQSGRDELREILIK SHMV 50 VWKPSPQVTVRFPD-SD-FKVYRYNAVLDPLVTALLGAFDTRNRIIEVEN TMV-OM S34858 VWKPSPQVTVRFPD-SD-FKVYRYNAVLDSLVTALLGAFDTRNRIIDVEN VWKPSPQVTVRFPD-SD-FKVYRYNAVLDPLVTALLGAFDTRNRIIDVEN S34857 VWKPSPQVTVRFPD-SD-FKVYRYNAVLDPLVTALLGAFDTRNRIIDVEN S34856 TMV-ER VWKPSPQVTVRFPD-RD-FKVYRYNAVLDPLVTALLGAFDTRNRIIEVEN VWKPSPOVTVRFPD-RD-FKVYRYNAVLDPLVTALLGAFDTRNRIIEVEN TMV-06 VWKPSPQVTVRFPD-SD-FKVYRYNAVLDPLVTALLGAFDTRNRIIEVEN TMV VWKPFPQSTVRFPG-DV-YKVYRYNAVLDPLITALLGTFDTRNRIIEVEN TMV-DA VWKPFPQSTVRFPG-DV-YKVYRYNAVLDPLITALLGAFDTRNRIIEVEN TOMV-L VWKTIPTATVRFPA-TG-FKVFRYNAVLDSLVSALLGAFDTRNRIIEVEN TOMV-KR AWKPVPSMTVRFPA-SD-FYVYRYNSTLDPLITALLNSFDTRNRIIEVDN **TMGMV** LFKTVPTRTNRFNDGENGFRVFRYNSTLDPLISALMNSFDTRNRIIEVDN TMV-OB VWKTIPTATVRFPA-TG-FKVFRYNAVLDSLVSALLGAFDTRNRIIEVEN **PMMV** LFKTVPTRTIRFSDGENGFRVFRYNSTLDPLITALLNSFDTRNRIIETEN **PKMMV** ORSV VWOPVPTLTSRFPAGAGYFRVYRYDPILDPLITFLMGTFDTRNRIIEVEN VWQPVPTLASRFPAGAGYFRDYRYDPILDPLITFLMGTFDTRNRIIEVEN ORSV-F CR-TMV LLSAVVAPSQRFPE-TG-SRVYVNSAVIKPLYEALMKSFDTRNRIIETEE TVCV LLSAVVTPSQRFPD-TG-SRVYVNSAVIKPLYEALMKSFDTRNRIIETEE LLSTIVAPNQRFPD-TG-FRVYVNSAVIKPLYEALMKSFDTRNRIIETEE AAB08579 LLSTIVAPNQRFPD-TG-FRVYVNSAVIKPLYEALMKSFDTRNRIIQTEE HRMV.GER LLSTIVAPNQRFPD-TG-FRVYVNSAVIKPLYEALMKSFDTRNRIIETEE HRMV.JAP WASABI LLSAIVTPNORFPE-TG-YRVYVNSAVLKPLYEALMKSFDTRNRIIETEE

Tobamovir	us Coat ProteinAlignment	
TMV-CG	LLSAIVTPNQRFPD-TG-YRV ISAVLKPLYESLMKSFDTRNRIIETEE	
CRMV	LLSAIVTPNQRFPE-AG-YRVYINSAVLKPLYESLMKSFDTRNRIIETEE	
RMV-SH	LLSAIVTPNQRFPE-TG-YRVYINSAVLKPLYESLMKSFDTRNRIIETEE	
AAD56047	LLSAIVTPNQRFPE-TG-YRMYINSAVLKPLYESLMKSFDTRNRIIETEE	
AAD20292	LLSAIVTPNQRFPE-SG-YRVYINSAVLKPLYEALMKSFDTRNRIIETEE	
CGMMV	LPSSVVDINSRFPD-AG-FYAFLNGPVLRPIFVSLLSSTDTRNRVIEVVD	
CGMMV-W	LPSSVVDINSRFPD-AG-FYAFLNGPVLRPIFVSLLSSTDTRNRVIEVVD	
C-CGMMV	LLTSVASLNSRFPA-NE-FFVWSRESRIAAIIDSLLSALDSRNRAIEVEN	
CFMMV	LLTTVASPRSRFPA-EG-FFVWSRESRIAAILDSLLSALDSRNRAIEVEN	
YCGMMV	LLTSVASPKSRFPA-GE-AFVWSRESRIAAILDSLLSALDSRNRAIEVEN	
KGMV	LLTSVASLNSRFPA-NE-FFVWSRESRIAAIIDSLLSALDSRNRAIEVEN	
ZGMV	LLSSVASPTSQFPS-GV-FYVWSRESRIAALIDSLFGALDSRNRAIEVEN	
SHMV	SQVSVVSPISRFPAEPA-YYIYLRDPSISTVYTALLQSTDTRNRVIEVEN	
mar ov	100	
TMV-OM	QANPTTAETLDATRRVDDATVAIRSAINNLVVELIRGTGSYNRSSFESSS	
S34858	QANPTTAETLDATRRVDDATVAIRSAINNLIVELIRGTRSYNRSSFESSY	
S34857	QANPTTAETLDATRRVDDATVAIRSAINNLIVELIRGTRSYNRSSFESSS OANPMTAETLDATRRVDDATVAIRSAINNLIVELIRGTGSYNRSSFESSS	
S34856	QANPMTAETLDATRRVDDATVAIRSAINNLIVELIRGIGSINKSSFESSS QANPTTAETLDATRRVDDATVAIRSAINNLIVELIRGTGSYNRSSFESSS	
TMV-ER	QANPTTAETLDATRRVDDATVAIRSAINNLTVELIRGIGSINKSSFESSS QANPTTAETLDATRRVDDATVAIRSAINNLMVELIRGIGSYNRSSFESSS	
TMV-06 TMV	QANPTTAETLDATRRVDDATVAIRSAINNLIVELIRGTGSYNRSSFESSS	
TMV-DA	QQSPTTAETLDATRRVDDATVAIRSAINNLVNELVRGTGLYNQNTFESMS	
TOMV-L	QQSPTTAETLDATRRVDDATVAIRSAINNLVNELVRGTGLYNQNTFESMS	
TOMV-KR	PQNPTTAETLDATRRVDDATVAIRASISNLMNELVRGTGMYNQALFESAS	
TMGMV	QPAPNTTEIVNATQRVDDATVAIRASINNLANELVRGTGMFNQAGFETAS	
TMV-OB	PANPNTSEVASATQRVDDATVNIRACINNLMNELVRGTGMMNTASFETVS	
PMMV	PONPTTAETLDATRRVDDATVAIRASISNLMNELVRGTGMYNQALFESAS	
PKMMV	PANPNTAEIASATQRVDDATVSIRACINNLMNELARGTGMLNTVSFETIS	
ORSV	PONPTTTETLDATRRVDDATVAIRSAINNLLNELVRGTGMYNQVSFETIS	
ORSV-F	PQNPTTTETLDATRRVDDATVAIRSAINNLLNELVRGTGMYNQVSFETMS	
CR-TMV	ESRPSASEVRNATQRVDDATVSIRSQIQLLLSELSSGHGYMNRAEFEAL-	
TVCV	ESRPSASEVANATORVDDATVAIRSQIQLLLSELSNGHGYMNRAEFEAL-	
	9 ESRPSASEVANATQRVDDATVAIRSQIQLLLNELSNGHGYMNRAEFEAI-	
HRMV.GER	QSRPSASQVANATQRVDDATVAIRSQIQLLLNELSNHGGYMNRAEFEAI-	
HRMV.JAP	ESRPSASOVADATORVDDATVAIRSQIQLLLNELSNHGGYMDRAQFEAI-	
WASABI	ESRPSASEVANATQRVDDATVAIRSQIQLLLSELSSGHGLMNRAEFEVL-	
TMV-CG	ESRPSASEVANATQRVDDATVAIRSQIQLLLNELSNGHGLMNRAEFEVL-	
CRMV	ESRPSASEVANATQRVDDATVAIRSQIQLLLNELSNGHGLMNRAEFEVL-	
RMV-SH	ESRPSASEVANATQRVDDATVAIRSQIQLLLNELSNGHGLMNRAEFEVL-	
AAD56047	ESRPSASEVANATQRVDDATVAIRSQIQLLLNELSNGHGLMNRAEFEVL-	
AAD20292	ESRPSASEVANATQRVDDATVAIRSQIQLLLNELSNGHGLMNRAEFEVL-	
CGMMV	PSNPTTAESLNAVKRTDDASTAARAEIDNLIESISKGFDVYDRASFEAAF	
CGMMV-W	PSNPTTAESLNAVKRTDDASTAARAEIDNLIESISKGFDVYDRASFEAAF	
C-CGMMV	PSNPSTGEALNATKRNDDASTAAHNDIPLLLAALNDGVGVFDSASFESAF	
CFMMV	PSNPSTSEALNATKRNDDASTAAHNDIPQLISALNDGAGVFDRASFESQF	
YCGMMV	PSNPSTGEALNATKRNDDASTAAHNDIPLLLAALNDGVGVFDTASFESAF	
KGMV	PSNPSTGEALNATKRNDDASTAAHNDIPLLLAALNDGVGVFDSASFESAF	
ZGMV	PSNPSTGEALNAVKRNDDASTAAHNDIPQILSALNEGAGVFDRASFESAF	
SHMV	STNVTTAEQLNAVRRTDDASTAIHNNLEQLLSLLTNGTGVFNRTSFESAS	
	150	
TMN - OM	150 GLVWNSGPA	
TMV-OM	CLVWNSGPA	

GLVWTSGPA S34858 GLVWTSGPA S34857 S34856 GLVWTSGPA GLVWTSGPA TMV-ER TMV-06 GLVWTSGPA ${\tt TMV}$ GLVWTSGPA TMV-DA GLVWTSAPA TOMV-L GLVWTSAPA TOMV-KR GLTWATTP? TMGMV GLVWTTTPA TMV-OB NLTWTTTTT

GLTWATTP?
NLTWTTAAT
GLTWTSS??
GLTWTSS??
-VPWTTAAA
-LPWTTAPA
-LPWTTAPA
-LPWTTAPA
-LPWTTAPA
-IPWATAPA
-LPWTTAPA
-LPWATAPA
-LPWATAPA
-LPWATAPA
-LPWTTAPA
SVVWSEATT
SVVWSEATT
GLTWTASAT
GLVWTAASS
GLTWTASSS
GLTWTASAT
GLVWTAGSS
GLTWLVTTT

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TMV-KR TMV-Rak TMV-vul TOMV **PMMV TMGMV** TMV-OB <u>ORSV</u> TVCV CR-TMV RMV-SH CRMV TMV-CG <u>CGMMV</u> CGMMV - W **CFMMV**

YCGMMV

SHMV

MAYTOTATTSALLDTVRGNNSLVNDLAKRRLYDTAVEEFNARDRRPKVNF MAYTQTATTSALLDTVRGNNSLVNDLAKRRLYDTAVDEFNARDRRPKVNF MAYTQTATTSALLDTVRGNNSLVNDLAKRRLYDTAVEEFNARDRRPKVNF MAYTQTATSSALLETVRGNNTLVNDLAKRRLYDTAVDEFNARDRRPKVNF MAYTQQATNAALASTLRGNNPLVNDLANRRLYESAVEQCNAHDRRPKVNF MAHIQSIISNALLESVSGKNTLVNDLARRRMYDTAVEEFNARDRRPKVNF MAHIQQSMQGALLDTVRGQNSLVNDLAKRRLYDTAVEEFNAKDRRPKINF MAHFQQTMNTKVTEAGIGRNSLINDLAQRRVYDKPVEELNHRSRRPKVNF MAQFQQTIDMQTLQAAAGRNSLVNDLASRRVYDNAVEELNARSRRPKVHF MAQFQQTIDMQTLQAAAGPNSLVNDLASRRVYDNAVEELNARSRRPKVHF MAQFQQTVNMQTLQAAAGRNSLVNDLASRRVYDNAVEELNARSRRPKVHF MAOFQOTVNMQTLQAAAGRNSLVNDLASRRVYDNAVEELNARSRRPKVHF MAOFOOTVNMQTLQAAAGRNSLVNDLASRRVYDNAVEELNARSRRPKVHF MANINEOINNORDAAASGRNNLVSQLASKRVYDEAVRSLDHQDRRPKMNF MANINEQINNQRDAAASGRNNLVSHLASKRVYDEAVRSLDHQDRRPKMNF MANITOHINDTREAAAAGRNPLVAQLASKRVYDEAVKSLDSQDKRPKVNF MANITOOIIDTREAAAAGRNPLIAQLASKRVYDEAVKSLDTQDKRPKVNF ---MSTSTLINKAQTNSCGDVGVVDLLKRKVYDDTVKTMQGLDRRAKYRL

51

TMV-KR TMV-RAK TMV TOMV PPMV **TMGMV** TMV-OB ORSV TVCV CR-TMV RMV-SH CRMV TMV-CG **CGMMV** CGMMV-W **CFMMV**

YCGMMV SHMV SKVISEEQTLIATRAYPEFQITFYNTQNAVHSLAGGLRSLELEYLMMQIP SKVISEEQTLIATRAYPEFQITFYNTQNAVHSLAGGLRSLELEYLMMQIP SKVISEEQTLIATRAYPEFQITFYNTQNAVHSLAGGLRSLELEYLMMQIP SKVVSEEQTLIATKAYPEFQITFYNTQNAVHSLAGGLRSLELEYLMMQIP LRSISEEQTLIATKAYPEFQITFYNTQNAVHSLAGGLRSLELEYLMMQIP SKTISEEOTLLVSNAYPEFQITFYNTQNAVHSLAGGLRALELEYLMLQVP SKSINEEOTLIVSOAYPEFQITFYNTQLAVHSLAAGLRSLELEYLMMQVP SKVISQEQIIQATNAYAEFEITFYNTQLAVHSMAGGLRALELEYRRMQIP SKAVSTEQTLIATNAYPEFEISFTHTQSAVHSLAGGLRSLELEYLMMQVP SKAVSTEOTLIATNAYPEFEISFTHTQSAVHSLAGGFRSLELEYLMMQVP SKSVSTEQTLLASNAYPEFEISFTHTQHAVHSLAGGLRTLELEYLMMQVP SKSVSTEQTLLASNAYPEFEISFTHTQQAVHSLAGGLRTLELEYLMMQVP SKSVSTEQTLLASNAYPEFEISFTHTQQAVHSLAGGLRTLELEYLMMQVP SRVVSTEHTRLVTDAYPEFSISFTATKNSVHSLAGGLRLLELEYMMMQVP SRVVSTEHTRLVTDAYPEFSISFTATKNSVHSLAGGLRLLELEYMMMQVP ARVLTTEOTRKVTESYPEFSISYTASALSVHSLAGGLRYLEGEYLMMQVP SRVLSTEQMRVVTENYPEFSVSYTGSALSVHSLAGGLRYLEGEYLMMQVP NQCLGPEQCRTVRGGYPEFQIEFTGASNTSHAMAAGLRGLELEYLYTLVP

101

TMV-KR
TMV-RAK
TMV
TOMV
PPMV
TMGMV
TMV-OB
ORSV
TVCV
CR-TMV
RMV-SH
CRMV
TMV-CG
CGMMV

CGMMV-W

CFMMV

SHMV

YCGMMV

YGSLTYDIGGNFASHLFKGRAYVHCCMPNLDVRDIMRHEGQKDSIELYLS YGSLTYDIGGNFASHLFKGRAYVHCCMPNLDVRDIMRHEGQKDSIEL - - -YGSLTYDIGGNFASHLFKGRAYVHCCMPNLDVRDIMRHEGOKDSIELYLS YGSLTYDIGGNFASHLFKGRAYVHCCMPNLDVRDIMRHEGQKDSIELYLS YGSTTYDIGGNFAAHMFKGRDYVHCCMPNMDLRDVMRHNAQKDSIELYLS YGSPTYDIGGNFAAHLFKGRDYVHCCMPNLDIRDIMRHEGQKDSIEMYLS YGSLTYDIGGNFAAHLFKGRDYVHCCMPNLDLRDIMRHENQKDSVATYLS FGSITYDIAGNFSAHIYKGRDYVHSCMRNLDIRDVARHINQQDTVSSYVA FGSLTYDIGGNFSAHLFKGRDYVHCCMPNLDVRDIARHEGHKEAIYSYVN FGSLTYDIGGNFSAHLFKGRDYVHCCMPNLDVRDIARHEGHKEAIHSYVN FGSLTYDIGGNFAAHLFKGRDYVHCCMPNLDVRDIARHEGHKEAIFSYLS FGSLTYDIGGNFAAHLFKGRDYVHCCMPNLDVRDIARHEGHKEAIFSYLS FGSLTYDIGGNFAAHLFKGRDYVHCCMPNLDVRDIARHEGHKEAIFSYIS YGSPCYDIGGNYTQHLFKGRSYVHCCNPCLDLKDVARNVMYNDMITQHVQ YGSPCYDIGGNYTOHLFKGRSYVHCCNPCLDLKDVARNVMYNDVVTQHVQ YGSPVYDIGGNYSQHMLKGRAYVHCCNPCLDLKDIARNEMYKDAIDRYVH YGSPCHYIGGNYSQHMLKGRSYVHCCNPCLDLKDVARNEMYKDAIERYVT YGAVSYDIGGNFPAHMMKGRSYVHCCNPALDARDLARNENYRISIENYLS

TMV-KR	RLERG'	KTVPNFQKEAFDRYAELPEDAVCHNTF
TMV-RAK	-LDRGG	KTVPNFQKEAFDRYAEFPEDAVCHNTF
TMV	RLERGG	KTVPNFQKEAFDRYAEIPEDAVCHNTF
TOMV	RLERGN	KHVPNFQKEAFDRYAEMPNEVVCHDTF
PPMV	KLAQKK	KVIPPYQKPCFDKYTDDPQSVVCSKPF
TMGMV	RLSRSN	KVIPEFQREAFNRYAEAPNEVCCSKTF
TMV-OB	RLKARN	KVLPAFQQEAFQRYSERSDEVVCNNTF
ORSV	RLERSK	RGLPVFQQSAFNKYMSDPDAVCSDKRF
TVCV	RLKRQQ	RPVPEYQRAAFNNYAENPHFVHCDKPF
CR-TMV	RLKRQQ	RPVPEYQRAAFNNYAENPHFVHCDKPF
RMV-SH	RLDRQK	RPVPEYQRAAFYNYAENPHFVHCDRPF
CRMV	RLDRQR	RPVPEYQRAAFHNYAENPHFVHCDRPF
TMV-CG	RLDRQR	RPVPEYQRAAFNNYAENPHFVHCDRPF
CGMMV	RHKGSCGC	RPLPTFQIDAFRRYDSSPCAVTCSDVF
CGMMV-W	RHKGSGGC	RPLPTFQIDAFRRYDNSPCAVTCSDVF
CFMMV	KKREAPRSNAWRARAESVQEIKD	GRLPSWQIDAFQRYKDCPRAVTCNDVF
YCGMMV	KKRDGPRSVAWRSQAESSQETKF	AGLPSWQMDAFRRYHSDPSSVTCPDVF
SHMV	RFEDKSGDYCQWQRKKPKVS	KPLPRYQKACFDRYNEDPEHVTCSETF

201

TMV-KR QTMRHQPMQQSGRVYAIALHSIYDIPADEFGAALLRKNVHTCYAAFHFSE TMV-RAK QTCEHQPMQQSGKVYAIALHSIYDIPADEFGAALLRKNVHTCYAAFHFSE TMV QTMRHQPMQQSGRVYAIALHSIYDIPADEFGAALLRKNVHTCYAAFHFSE TOMV QTCRHSQECYTGRVYAIALHSIYDIPADEFGAALLRKNVHVCYAAFHFSE QHCEGV-SHCTDKVYAVALHSLYDIPADEFGAALLRRNVHVCYAAFHFSE PPMV **TMGMV** QDCRIHPPENSGRRYAVALHSLYDIPVHEFGAALISKNIHVCYAASILAE TMV-OB OCCESNRYSSGGRVYAISLHSLYDIPADELGAALLRKNVHTLYAAFHFAE ORSV QECSYS-VDLPGKTYAVGLHSIYDIPADEFGAALLRKDVHICYAAFHISE TVCV QQCELT-TAYGTDTYAVALHSIYDIPVEEFGSALLRKNVKTCFAAFHFHE CR-TMV OOCELT-TANGTDTYAVALLSIYDIPVEEFGSALLRKNVKTCFAAFHFHE QQCEIS-TVNGADTYAIALHSIYDIPADEFGAALLRKNVKICYAAFHFHE RMV-SH CRMV QQCELS-TVNRWDTYA1ALHS1YD1PADEFGAALLRKNVK1CYAAFHFHE TMV-CG QQCKLS-AANGADTYAIALHSIYDIPVDEFGAALLRKNVKICYAAFHFHE **CGMMV** QECSYD-FGSGRDNHAVSLHSIYDIPYSSIGPALHRKNVRVCYAAFHFSE CGMMV-W QECSYD-SGSGGDNHAVSLHSIYDIPYSSIGPALHRKNVRVCYAAFHFSE QECQYE-HTRRGDRYAVALHSIYDIPFEQIGPALLRKNIKVLFAAFHFSE **CFMMV** QQCEHE-FSRGGDRYAVALHSIYDVPCEQIGPALLRKNIKVLFAAFHFSE YCGMMV SHMV EKCRISPPAERDDIYATSLHSLYDIPYQNLGPALARKRIKVLHAAFHFSE

251

NLLLEDSYVNLDEINACFSRDGDKLTFSFASESTLNYCHSYSNILKYVCK TMV-KR TMV-RAK NLLLEDSYVNLDEINACFSRDGDKLTFSFASESTLNYCHSFSNILKYVCK NLLLEDSYVNLDEINACFSRDGDKLTFSFASESTLNYCHSYSNILKYVCK TMV NLLLEDSHVNLDEINACFQRDGDRLTFSFASESTLNYSHSYSNILKYVCK TOMV PPMV NLLLEDSYVSLDDIGAFFSREGDMLNFSFVAESTLNYTHSYSNVLKYVCK **TMGMV** ALLLDOTEVTLNEIGATFKREGDDVSFFFADESTLNYSHKYKNILHYVVK TMV-OB ELLLEVSTVELPTIGGIFSRDGDKINFCFSNESTLNYSHSYSNLLKYVCK ORSV NLLLETTSAPLDEIGATKYKSGDRLSFFIQNESTLNYEHSYKNVIKYVCK TVCV NMLLDCDTVTLDEIGATFQKSGDNLSFFFHNESTLNYTHSFSNIIKYVCK NMLLDCDTVTLDEIGATFQRAGDNLSFFFHNESTLNYTHSFSNIIKYVCK CR-TMV RMV-SH NMLLDCDSVTLEDIGATFQRAGDKLNFFFHNESTLNYTHSFSNIIKYVCK NMLLDCDSVTLEDIGATFORAGDKLNFFFHNESTLNYTHSFSNIIKYVCK CRMV TMV-CG NMLLDCDSVTLEDIGATFQRAGDKLNFFFHNESTLNYTHSFSNIIKYVCK CGMMV ALLLGSPVGNLNSIGAQFRVDGDDVHFLFSEESTLHYTHSLENIKLIVMR CGMMV-W ALLLGSPVGNLNSIGAQFRVDGDDVHFLFSEESTLHYTHSLENIKLIVMR **CFMMV** ELLLGQSFGALPNIGAFFTVNGDSVEFQFEEESTLHYSHSFQNIRKIVTR DLLIGSEFGRLPNVGAFFSVDGDSVNFQFEDESTLHYTHSFSNIRKIVTR YCGMMV SHMV DLLLGASEGLLTOIGGTFORNGDVLTFSFLDESSLIYTHSFRNVFEYVTR

301

TMV-KR TYFPASNREVYMKEFLVTRVNTWFCKFSRIDTFLLYKGVAHKSVDSEQFY
TMV-RAK TYFPASNREVYMKEFLVTRVNTWFCKFSRIDTFLLYKGVAHKSVDSEQFY
TMV TYFPASNREVYMKEFLVTRVNTWFCKFSRIDTFLLYKGVAHKSVDSEQFY
TOMV TYFPASNREVYMKEFLVTRVNTWFCKFSRIDTFLLYKGVAHKGVDSEQFY

TYFPASSREVYMKEFLVTRV! PPMV FCKFSRLDTFVLYRGVYHRGVDKEQFY **TMGMV** SYFPASSRIVYFKEFLVTRVN. WFCKFTKVDTYILYKSVROVGCDSDQFY TYFPASNRFVYMKEFLITRVNTWFCKFTKLDTYTLYRGVYHRGCDQQEFY TMV-OB TFIPASNRFVYHKEFMCTRVNTWFCKFTKVDTYFLFRGVYTRGEDSEQFY ORSV TFFPASORFVYHKEFLVTRVNTWYCKFTRVDTFTLFRGVYHNNVDCEEFY TVCV CR-TMV TFFPASQRFVYHKEFLVTRVNTWYCKFTRVDTFTLFRGVYHNNVDCEEFY TFFPASQRYVYHKEFLVTRVNTWYCKFTRVDTFTLFRGVYRTSVDSEEFY RMV-SH TFFPASQRYVYHKEFLVTRVNTWYCKFTRVDTFTLFRGVYKTSVDSEEFY CRMV TFFPASQRYVYHKEFLVTRVNTWYCKFTRVDTFTLFRGVYRSSVDSEEFY TMV-CG TYFPADDRFVYIKEFMVKRVDTFFFRLVRADTHMLHKSVGHYS-KS----**CGMMV** TYFPADDRFVYIKEFMVKRVDTFFFRLVRADTHMLHKSVGHYS-KS----CGMMV-W TYFPASDRVVYVKEFMVKRVDTFFFRMVRVDTHMLHKSVGTYP-VC----**CFMMV** TFFPASDRVVYVKEFMVKRVDTFFFRMVRVDTHMLHKSVGQYQ-VS----YCGMMV TFFVACNRYAYMKEFRSRRVDTVFCSFIRIDTYCLYRSVFKDC-DEHV-F SHMV

35:

TAMEDAWHYKKTLAMCNSERILLEDSSSVNYWFPKMRDMVIVPLFDISLE TMV - KR TAMEDAWHYKKTLAMCNSERILLEDSSSVNYWFPKMRDMVIIPLFDISL-TMV-RAK TAMEDAWHYKKTLAMCNSERILLEDSSSVNYWFPKMRDMVIVPLFDISLE TMV TOMV KAMEDAWHYKKTLAMCNSERILLEDSSSVNYWFPKMRDMVIVPLFDISLE SAMEDAWHYKKTLAMMNSERILLEDSSSVNYWFPKMKDMVIVPLFDVSLQ PPMV **TMGMV EAMEDAFAYKKTLAMFNTERAIFRDTASVNFWFPKMKDMVIVPLFEGSIT** TMV-OB SAMEDAWHYKKTLAMLNSERIVLEDHSSVNYWFPKMKDMVIVPLFDVSLE ORSV TAMDEAWEYKKTLAMLNSERTIFRDRAAVNFRFPKVKDMVIVPLFDGSVT TVCV KAMDDAWHYKKTLAMLNAERTIFKDNAALNFWFPKVRDMVIVPLFDASIT CR-TMV KAMDDAWHYKKTLAMLNAERTIFKDNAALNFWFPKVRDMVIVPLFDASIT KAMDDAWEYKKTLAMLNSERTIFKDSAAMNFWFPKVRDMVIIPLFDASIT RMV-SH KAMDDAWEYKKTLAMLNSERTIFKDSAAINFWFPKVRDMVIIPLFDASIT CRMV TMV-CG KAMDDAWEYKKTLAMLNSERTIFKDSAAMNFWFPKVRDMVIIPLFDASIT -----KSEYFALNTPPIFQDKATFSVWFPEAK-KVLIPKFELSRF **CGMMV** -----KSEYFALNTPPIFODKATFSVWFPEAKRKVLIPKFELSRF CGMMV - W ------ATNYFSLKSSPIFODKATFSVWFPKAKSKVVIPIFKMQGF **CFMMV** -----KNDYYSLKSSPVFQDKATFSVWFPQAKSKVVIPLFEMQGF YCGMMV AAMDDAWEFKKKRVMLEASRPIFNDVAQFNVYFPNAKDKVCLPIFAVKSV SHMV

401

TMV-KR TSKR--TRKEVLVSKDFVFTVLNHIRTYQAKALTYANVLSFVESIRSRVI -----SRKEVLVSKDFVFTVLNHIRTYQAKALTYANVLSFVESIRSRVI TMV-RAK TSKR--TRKEVLVSKDFVFTVLNHIRTYQAKALTYANVLSFVESIRSRVI TMV TSKR--TRKEVLVSKDFVYTVLNHIRTYQAKALTYSNVLSFVESIRSRVI TOMV NEGKRLARKEVMVSKDFVYTVLNHIRTYOSKALTYANVLSFVESIRSRVI PPMV SKKM--TRSEVIVNRDFVYTVLNHIRTYOAKALTYONVLSFVESIRSRVI **TMGMV** TOKR--TKKEVIVSKDFVYTVLNHIRTYQAKALTYNNVLSFVESIRSRVI TMV-OB ORSV SGKM--KRREVMVNKDFVYTVLNHIRTYQDKALTYKNVLSFVESIRSRVI TVCV TGRM--SRREIMVNKDFVYTVLNHIKTYQAKALTYANVLSFVESIRSRVI CR-TMV TGRM--SRREVMVNKDFVYTVLNHIKTYQAKALTYANVLSFVESIRSRVI RMV-SH TGRM--SRREVLVNKDFVYTVLNHIKTYQAKALTYANVLSFVESIRSRVI CRMV TGRM--SRREVLVNKDFVYTVLNHIKTYOAKALTYANVLSFVESIRSRVI TGRM--SRREVLVNKDFVYTVLNHIKTYQAKALTYANVLSFVESIRSRVI TMV-CG **CGMMV** LSGNVKISR-MLVDADFVHTIINHISTYDNKALVWKNVQSFVESIRSRVI CGMMV-W LSGNVKISR-MLVDADFVHTIINHISTYDNKALVWKNVQSFVESIRSRVI FTGSIVAEK-MMIDASFIHTVINHICTYDNKALTWRNVQSFVESIRSRVV **CFMMV** FSGTLKSKK-MLVDATFIHTVINHICTYDNKALTWRNVQSFVESF-GLGC YCGMMV SGAPVTTRH-ILVEKDFYWTALNHILTYPDGKADFRGVMSFLESIRSRVV SHMV

451

TMV-KR INGVTARSEWDVDKSLLQSLSMTFYLHTKLAVLKDDLLISKFSLGSKTVC INGVTARSEWDVDKSLLOSLSMTFFLHTKLAVLKDDLLISKFSLGSKTVC TMV-RAK INGVTARSEWDVDKSLLQSLSMTFYLHTKLAVLKDDLLISKFSLGSKTVC TMV VMOT INGVTARSEWDVDKSLLQSLSMTFFLHTKLAVLKDDLLISKFALGPKTVS PPMV INGVTARSEWDVDKALLOSLSMTFFLQTKLAMLKDDLVVQKFQVHSKSLT INGVTARSEWDVDKAILQPLSMTFFLQTKLAALQDDIVMGKFRCLDKTTS **TMGMV** TMV-OB INGVTARSEWDVDKALLQSMAMTFFLITKLSMLKDELLVSKFTLSAKSVH ORSV MNGVTARSEWEVDKSVLQPLSMTFLLQTKLAEAKDQVVLKKFQKIDDTVT

INGVTARSEWDTDKAILGPL: TVCV FFLITKLGHVQDEIILKKFQKFDRTTN CR-TMV INGVTARSEWDTDKAILGPLAM (FFLITKLGHVQDEIILKKFQKFDRTTN RMV-SH INGVTARSEWDTDKAILGPLAMTFFLVTKLSHVQDEIVLKKFQKFDATAK CRMV INGVTARSEWDTDKAILGPLAMTFFLVTKLSHVODEIVLKKFOKFDATAK TMV-CG INGVTARSEWDTDKAILGPLAMTFFLVTKLSHVQDEIVLKKFQKFDATTK VNGVSVKSEWNVPVDQLTDISFSIFPLVKVRKVQIELMSDKVVIEARGLL **CGMMV** CGMMV-W VNGVSVKSEWNVPVDQLTDISFSIFLLVKVRKVQIELMSDKVVIEARGLL CFMMV VNGVSVRSEWDVPVELLTDISFTVFLLVKVKKTQIEIMSDKIVTQPQGLI YCGMMV MNGVSVRSEWDVPIEMLCDISFTVFLTVKV-KVQIEIMSEKIVTQPQGLL SHMV INGTTTASQWEVDKSQLKDIALSLLLIAKLEKLKISVIEKRIKIERQGLV

501

TMV-KR QHVWDEISLAFGNAFPSVKERLLNRKLIRVAGDALEIRVPDLYVTFHDRL TMV-RAK OHVWDEISLAFGNAFPSVKERLLNKKLIRAAGDALEIKVPDLYITFHDRL TMV OHVWDEISLAFGNAFPSVKERLLNRKLIRVAGDALEIRVPDLYVTFHDRL TOMV OHVWDEISLAFGNAFPSIKERLINRKLIKITENALEIRVPDLYVTFHDRL PPMV EYVWDEITAAFHNCFPTIKERLINKKLITVSEKALEIKVPDLYVTFHDRL **TMGMV** ELIWDEVGKFFGNVFPTIKERLVSRKILDVSENALKIKIPDLYVTWKDRF TMV-OB EHVWDEIKRGCGNMFPSLKESLLRKKLISGSAEELEIEVPDMYVTFHDRF ORSV NLFWKOISDAVGDLFPSIKERLISGGFVKVAEQSLQIKTPDEYITFADKL TVCV ELIWTSLCDALMGVIPSVKETLVRGGFVKVAEQALEIKVPELYCTFADRL CR-TMV ELIWTSLCDALMGVIPSVKETLVRGGFVKVAEQALEIKIPELYCTFADRL RMV-SH ELIWSSLCDALKGVIPSVKETLARGGFVKLAEESLEIKIPELYCTFTDRL CRMV ELIWSSLCDALKGVIPSVKETLARGGFVKLAEESLEIKIPELYCTFTDRL ELIWTSLCDALKGVIPSVKETLARGGFVKLAEESLEIKIPELYCTFTDRL TMV-CG **CGMMV** RRFADSLKSAVEGLGDCVYDALVQTGWFDTSSDELKVLLPEPFMTFSDYL CGMMV - W RRFADSLKSAVEGLGDCVYDALVQTGWFDTSSDELKVLLPEPFMTFSDYL **CFMMV** ERIVORVSEAFEGCTEAVQKALLTSGWFRTPADDLVLDIPELFMDFHDYL YCGMMV LRLAQKVSDAFEGCTATIHAALMSTGWFRCQADELVVEAPELFMDFHDFL SHMV SLLKEFLHGLLDEYTQTMAEWVVEKGWVKSVDQVLQVTIPDLVLNFRDHF

551

TMV-KR VTEYKASVDMPALDIRKKMEE--TEVMYNALSELSVLRESDKFDVDVFSO TMV-RAK VAEYKSSVDMPALDIRKRMEE - - TEVMYNALSELSVLRESDKFDVDVFSQ TMV VTEYKASVDMPALDIRKKMEE - - TEVMYNALSELSVLRESDKFDVDVFSQ VSEYKMSVDMPVLDIRKKMEE - - TEEMYNALSELSVLKNSDKFDVDVFSQ TOMV VKEYKSSVEMPVLDVKKSLEE--AEVMYNALSEISILKDSDKFDVDVFSR PPMV VAEYTKSEELPHLDIKKDLEE - - AEQMYDALSELSILKGADNFDIAKFKD **TMGMV** TMV-OB VAEYKASVEMPTIDISKDLSE - - AESYYSALSELSVLENSKDFDLEKFSR ORSV VMEYKATEELQHLDISKPLER - - AEKYYNALSELSVLKESDEFDITQFKN VLQYKKAEEFQSCDLSKPLEE - - SEKYYNALSELSVLENLDSFDLEAFKT TVCV CR-TMV VLQYKKAEEFQSCDLSKPLEE--SEKYYNALSELSVLENLDSFDLEAFKT RMV-SH VLEYKRTEEFQSCDLSKPLEE--SEKYYNALSELSVLENLDSFDLDAFKE CRMV VLEYKRTEEFQSCDLSKPLEE - - SEKYYNALSELSVLENLGSFDLDAFKE TMV-CG VLOYKMAEEFKSCDLSKPLEE - - SEKYYNALSELSVLENLDSFDLDGFKE **CGMMV** EGMYEADAKIERESVSELLAS - - GDDLFKKIDEIRNNYSGVEFDVEKFOE EGTYEADAKIERESVSELLAS - - GDDLFKKIDEIRNNYSGVEFDVEKFQE CGMMV - W CFMMV SGVFESRMLVLRRRTVEKCFKRFPTSFIRLYRKLCERYSGIEFDLEOVSD YCGMMV SAAWEADAKIEAANVESVLDA - - SDRLYTTVNELCERYSGIEFDLEKFTD SHMV RCEFRTSANVSEVNVSEHLVA - - TNEYYAKVSDLVDRNPTLAFDFEKFQD

601

TMV-KR MCQSLEVDPMTAAKVIVAVMSNESGLTLTFERPTEANVALALQDQ-EKAS TMV-RAK MCKSLEVDPMTAAKVIVAVMSNESGLTLTFERPTEANVAQALQDQ-EKAS TMV MCQSLEVDPMTAAKVIVAVMSNESGLTLTFERPTEANVALALQDQ-EKAS MCQSLEVDPMTAAKVIVAVMSNESGLTLTFEQPTEANVALALQDS-EKAS TOMV MCNTLGVDPLVAAKVMVAVVSNESGLTLTFERPTEANVALALQPTITSKE PPMV **TMGMV** MCKALDVSPDVAARVIVAVAENRSGLTLTFDKPTEENVAKALKSTASEAV TMV-OB MCAINCVNPDIAAKIVVAVLSNESGVTLPFKEPTEGNMAEAMKSGEKDEV ORSV LCEEKDIAPDVLAKVIVPIMKNE--LTLPFNNPTPEALSDALSPLPKDLD LCQQKNVDPDMAAKVVVAIMKSE--LTLPFKKPTEEEISESLKPGEGSCA TVCV CR-TMV LCQQKSVDPDMAAKVVVAIMKCE--LTLPFKKPTEEEISESLKTGEGTSA $\verb|LRQKKNVDPDVAAKVMVAIMNSE--LTLPFKKPTEEEVAEALSGEVVQDE|$ RMV-SH CRMV LCQKKNVDPDVAAKVVVAIMNSE--LTLPFKKPTEEEVAEALSGEVVQDE

TMV - CG	LCQKKNVDPDVAAKVVVAIMLTLPFKKPTEEEIAEALSGEVKQSE
CGMMV	FCKELNVNPMLIGHVIEAIFSQKAGVTVTGLGTLSPEMGASVALSSTSVD
CGMMV-W	FCKELNVNPMLIGHVIEAIFSQKAGVTVTGLGTLSPEMGASVALSNTSVD
CFMMV	FCHHHDVNPALVGPVIEAIFSQTAGITVTGLSTKSVEWAAAEALAPTSVD
YCGMMV	FCHHHDVNPSLIGTVIEAIFSQSAGITVTGLQAKSLEWAAAEALAP
SHMV	YCEKLGVDIDTVTELIDAISTGRAGITLDHTDDKEEQLPRTLAGSSSYLE

651

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TMV - KR	EGALVVTSR-EVEEPSM
TMV-RAK	EGALVVTSR-EVEEPSM
TMV	EGALVVTSR-EVEEPSM
TOMV	DGALVVTSR-DVEEPSI
PPMV	EGSLKIVSS-DVGESSI
TMGMV	VCLEPTSEEVNVNKFSI
TMV-OB	LTLGSQTDNTDLTSKSM
ORSV	MRFSLLKLSTCAPFPSV
TVCV	EHKEVLSLQNDAPFPCV
CR-TMV	EHKDVLSLQNDAPFPCV
RMV-SH	GLSLSNNAPFPCV
CRMV	GLRLSNKAPFPCV
TMV-CG	GLSLSNNAPFPCV
CGMMV	TCEDMDVTEDMEDIVLM
CGMMV-W	TCEDMDVTEDMEDIVLM
CFMMV	MDCDSDDEELEQKFPNL
YCGMMV	VDDDMDCSSDEEDAAPH
SHMV	EEPSDDLVCLSDKAIVN

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Appendit G

• D13367 Gb(84)_vi:MTVCP Tobacco mosaic virus CP gene. 7/94 474bp.

• D13438 Em(40)_vi:MTVGRNA Gb(84)_vi:MTVGRNA Tobacco mosaic virus genomic RNA. 12/93 6,507bp.

 <u>D17458</u> Em(40)_vi:MTV30KP Gb(84)_vi:MTV30KP Tobacco mosaic virus (TMV) RNA for 30K protein, complete cds. 3/94 795bp.

D38444 Em(44)_vi:Mtvcg Gb(90)_vi:Mtvcg Tobacco mosaic virus RNA. 10/94 6,303bp.

• J02412 Em(40)_vi:TO30KOM Gb(84)_vi:MTV30KOM tobacco mosaic virus 30k protein gene. 4/90 961bp.

• <u>J02413</u> Em(40)_vi:TOC30KCP Gb(84)_vi:MTV30KCP tobacco mosaic virus(cowpea strain) 30k & coat protein genes. 4/90 1,800bp.

• <u>J02415</u> Gb(84)_vi:MTVVCG Tobacco mosaic virus (strain vulgare), complete genome. 9/88 6,395bp.

• <u>L11665</u> Em(40)_vi:MTVNGHYPE Gb(84)_vi:MTVNGHYPER Tobacco mosaic virus RNA. 8/93 6,506bp

• L35073 Gb(84)n:MTVCOATPRA Tobacco mosaic virus coat protein, complete cds. 8/94 678bp.

• <u>L35074</u> Gb(84)n:MTVCOATPRO Tobacco mosaic virus coat protein, complete cds. 8/94 680bp.

• M19101 Em(40)_sy:AGVCHY Gb(84)_sy:SYNRMTVCHY Tobacco mosaic virus/calf chymosin recombined mRNA, promoter and 5' end. 7/89 101bp.

• M19102 Em(40)_sy:AGVLSZ Gb(84)_sy:SYNRMTVLSZ Tobacco mosaic virus/chicken lysozyme recombined mRNA, promotor and 5' end. 7/89 107bp

 M19103 Em(40)_sy:AGVCAT Gb(84)_sy:SYNRMTVCAT Tobacco mosaic virus/plasmid pJII2 chloramphenicol transferase recombined mRNA, leader and 5'

• M19104 Em(40)_sy:AGVNTP Gb(84)_sy:SYNRMTVNTP Tobacco mosaic virus/plasmid pJII3 neomycin phosphotransferase II recombined mRNA, leader and

• M19105 Em(40)_sy:AGVGUSA Gb(84)_sy:SYNVGUSA Tobacco mosaic virus/plasmid pJII119 beta-glucuronidase recombined mRNA, leader and 5' end. 7

• M19106 Em(40)_sy:AGVGUSB Gb(84)_sy:SYNVGUSB Tobacco mosaic virus/plasmid pJII139 beta-glucuronidase recombined mRNA, leader and 5' end. 7

 M24809 Em(40)_vi:TOBMTVGT Gb(84)_vi:MTVGTAMV tobacco mosaic virus RNA, 3' end. 2/90 72bp.

• M24955 Em(40)_vi:MTVU1RAA Gb(84)_vi:MTVU1RAA Tobacco mosaic virus (U1) omega RNA. 9/90 70bp.

• M24992 Gb(84)_vi:MTVU2RAA Tobacco mosaic virus (U2) omega RNA. 9/89 93bp.

• V01405 Em(40)_vi:TOTMV1 Gb(84)_vi:TOTMV1 Tobacco mosaic virus (TMV) RNA 5' coding region (nucleotides 69 to 236). 7/89 168bp.

• <u>V01407</u> Em(40)_vi:TOTMV3 Gb(84)_vi:TOTMV3 Two tobacco mosaic virus genes (viral transport and coat protein). 9/93 961bp.

• <u>V01408</u> Em(40)_vi:TOTMV4 Gb(84)_vi:TOTMV4 Tobacco mosaic virus genome (variant 1). 7/83 6,395bp

• <u>V01409</u> Em(40)_vi:TOTMV5 Gb(84)_vi:TOTMV5 Tobacco mosaic virus genome (variant 2). 7/83 6,398bp.

• <u>X00052</u> Em(40)_vi:TOTMV6 Gb(84)_vi:TOTMV6 Tobacco mosaic virus (TMV) common strain OM. 5'-terminal region. 6/85 275bp.

• X00053 Em(40)_vi:TOTMV7 Gb(84)_vi:TOTMV7 Tobacco mosaic virus tomato (TMV) strain L. 5'-terminal region. 6/85 278bp.

Appendix G (Continued)

• X02144 Em(40)_vi:TOTMV8 Gb(84)_vi:TOTMV8 Tobacco mosaic virus tomato strain (L) genome. 9/93 6,384bp.

X66047 Em(40)_vi:TMV54KDA Gb(84)_vi:TMV54KDA Tobacco Mosaic Virus RNA

for 54 kDa protein. 6/92 1,566bp.

• X68110 Em(40)_vi:TMVCG Gb(84)_vi:TMVCG Tobacco mosaic virus, complete genome. 10/92 6,395bp.

• X70882 Em(40)_vi:TMVPM2CP Gb(84)_vi:TMVPM2CP Tobacco mosaic virus PM2

mRNA for capsid protein. 7/93 765bp

• X70883 Em(40)_vi:TMVDT1CP Gb(84)_vi:TMVDT1CP Tobacco mosaic virus DT1 mRNA for capsid protein. 7/93 765bp.

• X70884 Em(40)_vi:TMVDT2CP Gb(84)_vi:TMVDT2CP Tobacco mosaic virus DT2

mRNA for capsid protein. 7/93 763bp.

• X70885 Em(40)_vi:TMVDT1GCP Gb(84)_vi:TMVDT1GCP Tobacco mosaic virus DT1G mRNA for capsid protein. 7/93 763bp.

Z29370 Em(40)_vi:TMVRPTPCP Gb(84)_vi:TMVRPTPCP Tobacco mosaic virus (Crucifer) genomic RNA for RNA-dependent RNA polymerase; 122K protein.

• M25782 Em(43)_vi:Sllcp Gb(89)_vi:Sllcp Satellite tobacco mosaic virus coat protein RNA, complete cds. 11/94 1,058bp.

Appendix H

- J02001 Gb(84)_vi:MAARNA23 alfalfa mosaic virus (Q strain) rna2 3' end. 2/85 228bp.
- J02003 Em(40)_vi:ALRNA3 Gb(84)_vi:MAARNA3 alfalfa mosaic virus rna 3 35kd protein leader sequence. 4/90 318bp.
- <u>J02005</u> Gb(84)_vi:MAARNA35 alfalfa mosaic virus (strain 425) rna3 5' end. 2/85 101bp.
- <u>K02702</u> Gb(84)_vi:MAACG2Z Alfalfa mosaic virus (strain 425 Leiden) RNA 2 of complete genome. 9/88 2,593bp.
- <u>K02703</u> Em(40)_vi:ALMRNA3 Gb(84)_vi:MAACG3Z Alfalfa mosaic virus (strain 425 Madison) RNA 3 of complete genome. 4/90 2,037bp
- <u>K03542</u> Em(40)_vi:MAARNA3L Gb(84)_vi:MAARNA3L Alfalfa mosaic virus RNA 3 encoding viral coat protein, complete.B. 4/90 2,142bp.
- L00161 Gb(84)_vi:MAARNA33 Alfalfa mosaic virus (strain Q) RNA 3, 3' end. 8/86 230bp
- <u>L00162</u> Em(40)_vi:ALMAARNA4 Gb(84)_vi:MAARNA4 Alfalfa mosaic virus (strain 425 Leiden) RNA 4 encoding viral coat protein. 5/94 964bp.
- <u>L00163</u> Em(40)_vi:ALMAACG1Z Gb(84)_vi:MAACG1Z Alfalfa mosaic virus (strain 425 Leiden) RNA 1 of complete genome. 5/94 3,644bp.
- L00164 Gb(84)_vi:MAARNA13 Alfalfa mosaic virus (strain Q) RNA 1. 8/86 226bp.
- M10826 Em(40)_vi:MAARNA01 Gb(84)_vi:MAARNA4AX Alfalfa mosaic virus (A1MV) RNA 4, 3' terminal fragment 29C. 7/91 91bp.
- M10851 Em(40)_vi:MAARNA4A Gb(84)_vi:MAARNA4A Alfalfa mosaic virus RNA 4, 5' terminal region. 7/89 74bp.
- M25004 Em(40)_vi:ALMAARNAA Gb(84)_vi:MAARNAA Alfalfa mosaic virus RNA 3 or 4, 3' end. 4/92 113bp.
- M25005 Em(40)_vi:ALMAARNAB Gb(84)_vi:MAARNAB Alfalfa mosaic virus RNA 2, 3' end. 4/92 103bp.
- M25006 Em(40)_vi:ALMAARNAC Gb(84)_vi:MAARNAC Alfalfa mosaic virus RNA 1, 3' end. 4/92 110bp.
- M25452 Em(40)_vi:ALMAARNA1 Gb(84)_vi:MAARNA4D Alfalfa mosaic virus RNA 4 RNA fragment. 4/92 62bp.
- M35975 Em(40)_vi:ALMAARNA Gb(84)_vi:MAARNA1A Alfalfa mosaic virus (strain AlMV-S) 5' end of RNA-1. 12/90 163bp.
- M35976 Em(40)_vi:ALMAAR01 Gb(84)_vi:MAARNA1B Alfalfa mosaic virus (strain AlMV-B) 5' end of RNA-1. 12/90 115bp.
- M36389 Em(40)_vi:ALMAAR02 Gb(84)_vi:MAARNA2A Alfalfa mosaic virus (strain AlMV-S) 5' end of RNA-2. 12/90 108bp.
- M36390 Em(40)_vi:ALMAAR03 Gb(84)_vi:MAARNA2B Alfalfa mosaic virus (strain AlMV-B) 5' end of RNA-2. 12/90 109bp.
- M36391 Em(40)_vi:ALMAAR04 Gb(84)_vi:MAARNA3B Alfalfa mosaic virus (strain AlMV-S) 5' end of RNA-3. 12/90 305bp.
- M36392 Em(40)_vi:ALMAAR05 Gb(84)_vi:MAARNA3C Alfalfa mosaic virus (strain AlMV-B) 5' end of RNA-3. 12/90 290bp.

• M59241 Em(40)_vi:ALMAA32K Gb(84)_vi:MAA32KDMP Alfalfa mosaic virus 32 kDa movement protein and coat protein RNA, complete cds. 8/92 2,188bp.

S55890 Em(40)_vi:S55890 Gb(84)_vi:S55890 RNA-3 coat protein homolog, alfalfa mosaic virus RNA-3 32K protein homolog (RNA-2) (raspberry bushy dwarf virus, Genomic RNA, 2231 nt).

• <u>U12509</u> Em(43)_vi:Am12509 Gb(89)_vi:Amu12509 Alfalfa mosaic virus NZ1 RNA4 coat protein mRNA, complete cds. 8/94 876bp.

• <u>U12510</u> Em(43)_vi:Am12510 Gb(89)_vi:Amu12510 Alfalfa mosaic virus NZ2 RNA4 coat protein mRNA, complete cds. 8/94 876bp.

 V00044 Em(40)_vi:ALALM1 Gb(84)_vi:ALALM1 5' end of alfalfa mosaic virus RNA 1. 5/94 61bp.

• V00045 Em(40)_vi:ALALM2 Gb(84)_vi:ALALM2 5' end of alfalfa mosaic virus RNA 2. 5/94 13bp.

V00046 Em(40)_vi:ALALM3 Gb(84)_vi:ALALM3 5' end of alfalfa mosaic virus RNA 3. 5/94 101bp.

• V00047 Em(40)_vi:ALALM4 Gb(84)_vi:ALALM4 Intercistronic junction in alfalfa mosaic virus RNA 3. 5/94 122bp.

• <u>V00048</u> Em(40)_vi:ALALM5 Gb(84)_vi:ALALM5 alfalfa mosaic virus RNA 4 coding for the coat protein. 5/94 881bp.

• V00049 Em(40)_vi:ALALM6 Gb(84)_vi:ALALM6 3' end of alfalfa mosaic virus RNA 1. 7/91 226bp.

 V00050 Em(40)_vi:ALALM7 Gb(84)_vi:ALALM7 3' end of alfalfa mosaic virus RNA 2. 7/91 228bp.

V00051 Em(40)_vi:ALALM8 Gb(84)_vi:ALALM8 3' end of alfalfa mosaic virus RNA 3. 7/91 230bp.

• V00052 Em(40)_vi:ALAM01 Gb(84)_vi:ALAM01 Alfalfa mosaic virus RNA 1 fragment. (Obtained after digestion with ribonuclease T1.). 5/94 8

• <u>V00053</u> Em(40)_vi:ALAM02 Gb(84)_vi:ALAM02 Alfalfa mosaic virus RNA 1 fragment. (Obtained after digestion with ribonuclease T1.). 5/94 6

• V00054 Em(40)_vi:ALAM03 Gb(84)_vi:ALAM03 Alfalfa mosaic virus RNA 1 fragment. (Obtained after digestion with ribonuclease T1.). 5/94 4

• V00055 Em(40)_vi:ALAM04 Gb(84)_vi:ALAM04 Alfalfa mosaic virus RNA 1 fragment. (Obtained after digestion with ribonuclease T1.). 5/94 4

V00056 Em(40)_vi:ALAM05 Gb(84)_vi:ALAM05 Alfalfa mosaic virus RNA 1 fragment. (Obtained after digestion with ribonuclease T1.). 5/94 4

• <u>V00057</u> Em(40)_vi:ALAM06 Gb(84)_vi:ALAM06 Alfalfa mosaic virus RNA 1 fragment. (Obtained after digestion with ribonuclease T1.). 5/94 3

• <u>V00058</u> Em(40)_vi:ALAM07 Gb(84)_vi:ALAM07 Alfalfa mosaic virus RNA 1 fragment. (Obtained after digestion with ribonuclease T1.). 5/94 3

• V00059 Em(40)_vi:ALAM08 Gb(84)_vi:ALAM08 Alfalfa mosaic virus RNA 1 fragment. (Obtained after digestion with ribonuclease T1.). 5/94 3

• V00060 Em(40)_vi:ALAM09 Gb(84)_vi:ALAM09 Alfalfa mosaic virus RNA 1 fragment. (Obtained after digestion with ribonuclease T1.). 5/94 2

• V00061 Em(40)_vi:ALAM10 Gb(84)_vi:ALAM10 Alfalfa mosaic virus RNA 1 fragment. (Obtained after digestion with ribonuclease T1.). 5/94 2

- V00062 Em(40)_vi:ALAM11 Gb(84)_vi:ALAM11 Alfalfa mosaic virus RNA 1 fragment. (Obtained after digestion with ribonuclease A.). 5/94 25
- <u>V00063</u> Em(40)_vi:ALAM12 Gb(84)_vi:ALAM12 Alfalfa mosaic virus RNA 1 fragment. (Obtained after digestion with ribonuclease A.). 5/94 19
- V00064 Em(40)_vi:ALAM13 Gb(84)_vi:ALAM13 Alfalfa mosaic virus RNA 1 fragment. (Obtained after digestion with ribonuclease A.). 5/94 19
- V00065 Em(40) vi:ALAM14 Gb(84) vi:ALAM14 Alfalfa mosaic virus RNA 1 fragment. (Obtained after digestion with ribonuclease A.). 5/94 18
- <u>V00066</u> Em(40)_vi:ALAM15 Gb(84)_vi:ALAM15 Alfalfa mosaic virus RNA 1 fragment. (Obtained after digestion with ribonuclease A.). 5/94 18
- <u>V00067</u> Em(40)_vi:ALAM16 Gb(84)_vi:ALAM16 Alfalfa mosaic virus RNA 1 fragment. (Obtained after digestion with ribonuclease A.). 5/94 15
- <u>V00068</u> Em(40)_vi:ALAM17 Gb(84)_vi:ALAM17 Alfalfa mosaic virus RNA 1 fragment. (Obtained after digestion with ribonuclease T1.). 5/94 9
- X00819 Em(40)_vi:ALAM19 Gb(84)_vi:ALAM19 Alfalfa mosaic virus (strain S) complete RNA 3 sequence. 9/93 2,055bp.
- X01572 Em(40)_vi:A1MVRNA2 Gb(84)_vi:A1MVRNA2 Alfalfa mosaic virus (A1M4) RNA 2. 7/91 2,593bp.
- M28374 Em(43)_vi:Maatbts7a Gb(89)_vi:Maatbts7a Alfalfa mosaic virus (clone 143) temperature-sensitive mutant Tbts7 RNA3 (coat protein-encodi
- M28375 Em(43)_vi:Maatbts7b Gb(89)_vi:Maatbts7b Alfalfa mosaic virus (clone 112) temperature-sensitive mutant Tbts7 RNA3 (coat protein-encoding), 5' end fragment.

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